



Europäisches Patentamt
European Patent Office
Office européen des brevets



(11) **EP 1 564 293 A1**

(12) **EUROPEAN PATENT APPLICATION**

(43) Date of publication:
17.08.2005 Bulletin 2005/33

(51) Int Cl.7: **C12N 15/12**, G01N 33/53,
A61K 49/00, A61K 31/70,
C12Q 1/68, C12N 5/00,
C12P 21/02, C07H 15/12

(21) Application number: **04076254.4**

(22) Date of filing: **20.04.1994**

(84) Designated Contracting States:
**AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL
PT SE**

(30) Priority: **20.04.1993 US 50559**

(62) Document number(s) of the earlier application(s) in
accordance with Art. 76 EPC:
94915396.9 / 0 697 893

(71) Applicant: **THE GENERAL HOSPITAL
CORPORATION
Boston, MA 02114 (US)**

(72) Inventors:
• **de la Monte, Suzanne M.
East Greenwich, CT 02181 (US)**

• **Wands, Jack R.
Waban, MA 02168 (US)**

(74) Representative: **Chapman, Paul William et al
Kilburn & Strode,
20 Red Lion Street
London WC1R 4PJ (GB)**

Remarks:

This application was filed on 26 - 04 - 2004 as a
divisional application to the application mentioned
under INID code 62. The sequence listing, which is
published as annex to the application documents,
was filed after the date of filing. The applicant has
declared that it does not include matter which goes
beyond the content of the application as filed.

(54) **Neural thread protein gene expression and detection of Alzheimer's disease**

(57) The present invention is directed to recombinant hosts expressing proteins associated with Alzheimer's Disease, neuroectodermal tumors, malignant astrocytomas, and glioblastomas. This invention is specifically directed to the recombinant hosts and vectors which contain the genes coding for the neuronal thread proteins. This invention is also directed to substantially

pure neural thread protein, immunodiagnostic and molecular diagnostic methods to detect the presence of neural thread proteins, and the use of nucleic acid sequences which code neural thread proteins in gene therapy.

EP 1 564 293 A1

Description**Statements as to Rights to Inventions Made Under Federally-Sponsored Research and Development**

5 **[0001]** The present invention was made with U.S. government support. Therefore, the U.S. government has certain rights in the invention.

Cross Reference to Related Applications

10 **[0002]** This is a continuation-in-part of U.S. Application Serial No. 08/050,559, filed April 20, 1993, the contents of which are fully incorporated by reference herein.

Field of the Invention

15 **[0003]** The present invention is in the field of genetic engineering and molecular biology. This invention is directed to recombinant hosts expressing novel proteins associated with Alzheimer's Disease, neuroectodermal tumors, malignant astrocytomas, and glioblastomas. This invention is specifically directed to the recombinant hosts and vectors which contain the genes coding for the neuronal thread proteins. This invention is also directed to substantially pure neural thread proteins, immunodiagnostic and molecular diagnostic methods to detect the presence of neural thread proteins, and the use of nucleic acid sequences which code for neural thread proteins in gene therapy.

Background of the Invention**Alzheimer's Disease**

25 **[0004]** Alzheimer's Disease (AD) is the most frequent cause of dementia in the United States, affecting over two million individuals each year. It is a degenerative brain disorder characterized clinically by loss of memory, confusion, and gradual physical deterioration. It is the fourth most common cause of death. The etiology of the disease is virtually unknown but has been attributed to various viruses, toxins, heavy metals, as well as genetic defects. The disease is at present incurable.

30 **[0005]** Until quite recently, AD was thought to account for relatively few of the cases generally classified as senile dementia. Other factors can lead to such a condition, including repetitious mild strokes, thyroid disorders, alcoholism, and deficiencies of certain vitamins, many of which are potentially treatable. It can be appreciated, then, that a diagnostic test specific for AD would be very useful for the clinical diagnosis and proper clinical treatment of subjects presenting with symptoms common to all of these conditions.

35 **[0006]** The brains of individuals with AD exhibit characteristic pathological accumulations of congophilic fibrous material which occurs as neurofibrillary tangles within neuronal cell bodies, and neuritic (or senile) plaques. Neurofibrillary tangles may also be found in the walls of certain cerebral blood vessels. The major organized structural components of neurofibrillary tangles are paired helical filaments. Qualitatively indistinguishable amyloid deposits also occur in normal aged brains but in much smaller numbers with restricted topographical distribution.

40 **[0007]** There has been considerable recent investigative activity regarding the characterization of proteins found in neuritic plaques and neurofibrillary tangles of AD and other neurologic diseases. One of the amyloid proteins initially described by Glenner *et al.* has been cloned and sequenced (Glenner *et al.*, *Biochem. Biophys. Res. Commun.* 120: 1131-1135 (1984); U.S. Patent No. 4,666,829). The A4 amyloid protein found in neuritic plaques and blood vessels has been determined to be a component of a 695 amino acid precursor; a protein postulated to function as a glycosylated cell surface receptor (Masters *et al.*, *Proc. Natl. Acad. Sci. USA* 82:4245-4249 (1985), Kang *et al.*, *Nature* 325: 733-736 (1987)). In addition, the amyloid protein has been postulated to function as a cell adhesion molecule and as a calcium ion channel protein (Hooper, J. *NIH Res.* 4: 48-54 (1992); Rensberger, *Wayward Protein Molecule May Be Elusive Killer of Brain Cells*, *The Washington Post*, January 25, 1993, §1, at A3 (1993)). The gene coding for A4 is located on chromosome 21 (Kang *et al.*, *ibid.*; Goldgaber *et al.*, *Science* 235:877-880 (1987); Tanzi *et al.*, *Science* 235: 880-885 (1987); St. George-Hyslop *et al.*,

45 **[0008]** *Science* 235:885-889 (1987)) but apparently is not linked to the familial form of the disease (Van Broekhoven *et al.*, *Nature* 329:153-155 (1987)). There appears to be little, if any, protein sequence homology between amyloid A4 and β protein, their higher molecular weight precursor, and pancreatic thread protein (PTP) (Gross *et al.*, *J. Clin. Invest.* 76:2115-2126 (1985)).

50 **[0009]** A number of other proteins thought to be associated with the disease have been described, including Ubiquitin, ALZ-50, microtubular-associated proteins τ and MAP2, and neurofilament protein (*see*, for example, Manetto *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4502-4505 (1988); Wolozin *et al.*, *Science* 232:648-651 (1986); Selkoe, *Neurobiol. Aging*

7:425-432 (1986); Perry *et al.*, in: *Alterations of the Neuronal Cytoskeleton in Alzheimer's Disease*, Plenum, New York, pp 137-149 (1987)). More recently, a serine protease inhibitor called α_1 -anti-chymotrypsin has been found in AD amyloid deposits (Abraham *et al.*, *Cell* 52:487-501 (1988)).

[0010] There is currently no useful diagnostic test for AD being practiced clinically. A definitive diagnosis is possible only postmortem, or during life through a brain biopsy, to reveal the presence of the characteristic plaques, tangles, paired helical filaments, and other cerebrovascular deposits which characterize the disorder. Such an invasive surgical procedure is inherently dangerous and is therefore rarely utilized. As a result, the clinical misdiagnosis of AD is estimated to be approximately 20%-30%.

Thread Proteins

[0011] The prototype thread protein molecule is pancreatic thread protein (PTP) which bears the unusual physical property of forming insoluble fibrils at neutral pH, but is highly soluble at acid or alkaline pH (Gross *et al.*, *supra*). PTP is highly abundant, synthesized by pancreatic acinar cells, and secreted into pancreatic juice in concentrations exceeding 1 mg/ml (*Id.*). An increased thread protein immunoreactivity has been demonstrated in brains with AD lesions, using monoclonal antibodies to PTP (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989)). In addition, a highly sensitive forward sandwich immunoradiometric assay was used to demonstrate that at least three distinct antigenic epitopes were shared between PTP and the related protein in the brain (*Id.*) Despite similarities, the pancreatic and neuronal forms of the thread protein are almost certainly distinct since the mRNA molecules and proteins differ in size, and many of the antigenic epitopes which are present in the pancreatic thread protein are not detectable in brain tissue (de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)).

[0012] The central nervous system form of the thread protein, designated hereafter as "neural thread protein" (NTP), has been identified in AD and Down's Syndrome brain tissue (Wands *et al.*, International Application Publication No. WO 90/06993). NTP has been found in all AD brains studied where characteristic neuropathologic changes of the disease exist (*Id.*). The saline-extractable soluble immunoreactivity shares has a molecular weight of approximately 17 to 20 kD (*Id.*).

[0013] Quantitative measurements of NTP immunoreactivity in various regions of AD brains revealed levels varying from 12 to 295 ng/gm tissue (Mean = 116 ng/gm tissue) compared to 1-11 ng/gm tissue (Mean = 5 ng/gm tissue) in comparable areas of control brains (*Id.*).

[0014] Immunocytochemistry performed with monoclonal antibodies directed against the pancreatic form of PTP demonstrated that NTP is localized within cells, within fine processes within the neuropil, or is extracellular in both AD and Down's Syndrome brains (*Id.*). Two types of cell contain NTP: neurons and astrocytes (*Id.*). The affected neurons are the large pyramidal type which typically contain the neurofibrillary tangles well known in AD brain (*Id.*).

[0015] That NTP accumulation within neurons is intrinsically important or integrally related to the evolution of AD lesions is corroborated by the presence of identical patterns of immunolabeling for NTP in Down's Syndrome brains, but not in control brains (*Id.*). It is important to note that the same structural abnormalities of AD occur in brains of all middle-age individuals with Down's syndrome, whether or not they are demented. There is also a higher incidence of AD in family members of Down's Syndrome patients. Moreover, the regional differences in the densities of NTP-containing neurons parallels the density distributions of neurofibrillary tangles in both AD and Down's Syndrome. This provides further evidence that NTP is germane to the pathophysiology of AD. Whether NTP accumulates within neuronal perikarya, as a result of aberrant cellular metabolism or transport is not yet known.

Summary of the Invention

[0016] A need exists for a definitive diagnostic test which can be performed on individuals suspected of having, or being at risk for AD. The present invention satisfies such needs and provides further advantages.

[0017] The manner in which these and other objects are realized by the present invention will be apparent from the summary and detailed description set forth below.

[0018] Unless defined otherwise, various terms used herein have the same meaning as is well understood in the art to which the invention belongs. All cited publications are incorporated herein by reference.

[0019] This invention is directed to recombinant hosts expressing novel proteins associated with Alzheimer's Disease, neuroectodermal tumors, malignant astrocytomas, and glioblastomas. This invention is specifically directed to the recombinant hosts and vectors which contain the genes coding for the neuronal thread proteins (NTP) having molecular weights of about 8 kDa, 14 kDa, 17 kDa, 21 kDa, 26 kDa or 42 kDa. This invention is also directed to the substantially pure neural thread proteins, immunodiagnostic and molecular diagnostic methods to detect the presence of neural thread proteins, and the use of nucleic acid sequences which code for neural thread proteins in gene therapy.

[0020] In particular, the invention includes a method for detecting and quantitating an NTP in a human subject, com-

prising:

- (a) contacting a biological sample from a human subject that is suspected of containing detectable levels of an NTP with a molecule capable of binding to the NTP; and
- (b) detecting the molecule bound to the NTP.

[0021] The invention additionally includes the method as above, wherein the binding molecule is selected from the group consisting of:

- (a) an antibody substantially free of natural impurities;
- (b) a monoclonal antibody; and
- (c) a fragment of (a) or (b).

[0022] The invention additionally includes the method as above, wherein the detecting molecule is detectably labeled and where a combination of such binding molecules is used.

[0023] The invention additionally includes a method for detecting the presence of a genetic sequence coding for an NTP in a biological sample using a polynucleotide probe derived from a recombinant human NTP of this invention.

[0024] The invention additionally includes a method for determining the presence of a condition in a human subject, said condition including, but not limited to, the group consisting of Alzheimer's Disease, the presence of neuroectodermal tumors, the presence of malignant astrocytomas, and the presence of gliomas.

[0025] The invention additionally includes a method of diagnosing the presence of AD in a human subject suspected of having AD which comprises:

- (a) incubating a biological sample from said subject suspected of containing an NTP with a molecule capable of identifying an NTP; and
- (b) detecting the molecule which is bound in the sample, wherein the detection indicates that the subject has AD.

[0026] The invention additionally includes a method of diagnosing the presence of neuroectodermal tumors in a human subject suspected of having neuroectodermal tumors which comprises:

- (a) incubating a biological sample from said subject suspected of containing an NTP with a molecule capable of identifying an NTP; and
- (b) detecting the molecule which is bound in the sample, wherein the detection indicates that the subject has neuroectodermal tumors.

[0027] The invention additionally includes a method of diagnosing the presence of a malignant astrocytoma in a human subject suspected of having a malignant astrocytoma which comprises:

- (a) incubating a biological sample from said subject, which is suspected of containing an NTP, in the presence of a binding molecule capable of identifying an NTP; and
- (b) detecting molecule which is bound in the sample. wherein the detection indicates that the subject has a malignant astrocytoma.

[0028] The invention additionally includes a method of diagnosing the presence of a glioblastoma in a human subject suspected of having a glioblastoma which comprises:

- (a) incubating a biological sample from said subject, which is suspected of containing an NTP, in the presence of a binding molecule capable of identifying an NTP; and
- (b) detecting molecule which is bound in the sample, wherein the detection indicates that the subject has a glioblastoma.

[0029] The invention additionally includes the methods as above, wherein a biological sample is removed a human subject prior to contacting the sample with the molecule.

[0030] The invention additionally includes the methods as above, wherein detecting any of the molecules bound to the protein is performed by *in situ* imaging.

[0031] The invention additionally includes the methods as above, wherein detecting of any of the molecule bound to the protein is performed by *in vivo* imaging.

[0032] The invention additionally includes the methods as above, wherein the biological sample is reacted with the

binding molecule in a manner and under such conditions sufficient to determine the presence and the distribution of the protein.

[0033] The invention additionally includes the methods as above, wherein a detectably labeled binding molecule of an NTP is administered to a human subject.

[0034] The invention additionally includes the methods as above, wherein the binding molecule is bound to the protein *in vivo*.

[0035] The invention additionally involves an NTP substantially free of any natural impurities and having a molecular weight of about 42 kDa.

[0036] The invention additionally involves an NTP substantially free of any natural impurities and having a molecular weight of about 26 kDa.

[0037] The invention additionally includes an NTP substantially free of any natural impurities and having a molecular weight of about 21 kDa.

[0038] The invention additionally includes an NTP substantially free of any natural impurities and having a molecular weight of about 17 kDa.

[0039] The invention additionally includes an NTP substantially free of any natural impurities and having a molecular weight of about 14 kDa.

[0040] The invention additionally includes an NTP substantially free of any natural impurities and having a molecular weight of about 8 kDa.

[0041] The present invention also particularly relates to the diagnostic methods recited above, wherein the immunoassay comprises two different antibodies bound to a solid phase support combined with a third different detectably labeled antibody in solution.

[0042] The invention is also directed to a method of producing an NTP, said method comprising:

(a) culturing a recombinant host comprising a human gene coding for said NTP; and

(b) isolating said NTP from said host.

[0043] Additionally, the invention is directed to a substantially pure NTP obtained by the such a process.

[0044] The invention is also directed to an 15- to 30-mer antisense oligonucleotide which is complementary to an NTP nucleic acid sequence and which is nonhomologous to PTP nucleic acid sequences, as well as pharmaceutical compositions comprising such oligonucleotides and a pharmaceutically acceptable carrier.

[0045] The invention is also directed to ribozymes comprising a target sequence which is complementary to an NTP sequence and nonhomologous to PTP nucleic acid sequences, as well as pharmaceutical compositions comprising such ribozymes and a pharmaceutically acceptable carrier.

[0046] The invention is also directed to a method of achieving pharmaceutical delivery of NTP molecules to the brain through acceptable carriers or expression vectors.

[0047] The invention is also directed to oligodeoxynucleotides that form triple stranded regions with the various NTP genes (nucleic acid sequences) and which are nonhomologous to PTP nucleic acid sequences, as well as pharmaceutical compositions comprising such oligodeoxynucleotides and a pharmaceutically acceptable carrier.

[0048] The invention is also directed to the therapeutic use of NTP-derived molecules or fragments thereof to modify or improve dementias of the Alzheimer's type of neuronal degeneration.

[0049] The invention is also directed to methods for the differential diagnosis of sporadic and familial Alzheimer's disease.

Brief Description of the Drawings

[0050]

Figures 1A-1J show neural thread protein immunoreactivity in CNS-derived tumors.

Figure 2 depicts a graph showing neural thread protein levels in PNET1, PNET2, A172, C6, and Huh7 hepatocellular carcinoma cells measured by a forward sandwich monoclonal antibody-based immunoradiometric assay (M-IRMA).

Figure 3 shows molecular size of neural thread proteins in SH-Sy5y, A172, and C6 cells demonstrated by immunoprecipitation and Western blot analysis using the Th9 monoclonal antibody.

Figure 4 shows molecular sizes of neural thread proteins in PNET1 cells (a) and C6 glioblastoma cells (b) demonstrated by pulse-chase metabolic labeling with ³⁵S-methionine, and immunoprecipitation with Th9 monoclonal antibody (Figure 4A). The molecular weights are 8, 14, 17, 21, 26 and 42 kDa (arrows).

Figures 5A-5E depict a series of five graphs showing the 21 kDa and 17 kDa neural thread proteins in SH-Sy5y, PNET1, A172, and C6 cells and the absence thereof in Huh7 cells by SDS-PAGE/M-IRMA.

Figure 6 depicts a gel showing that the 21 kDa neural thread protein in C6 glioblastoma cells is phosphorylated. Figure 7 depicts a bar graph showing altered neural thread protein expression in PNET1 cells with growth phase. Figures 8A-8F show altered phenotype of PNET1 cells with cessation of cell growth and overnight serum starvation. Figure 9 shows the 1-9a partial cDNA sequence, and Figure 9A shows a partial sequence of the second 5' anchor PCR product corresponding to the 5' region of the 1-9a cDNA (WP5' Sequence).
 Figure 10 shows alignment of partial sequences between 1-9a and human PTP and the Reg gene (the nucleic acid sequence corresponding to the genomic clone of human PTP).
 Figure 10A shows alignment between 1-9a and Exon 2 of the human Reg gene, and between the first 5' anchor PCR product of 1-9a (WP03-417) and Exon 2 and Reg.
 Figure 10B shows alignment between the 1-9a and its second 5' anchor PCR product (WP5') and AD 3-4 and AD 2-2 cDNAs.
 Figure 11A shows the partial nucleic acid and deduced amino acid sequences of the HB4 cDNA. Figures 11B and 11C show a protein hydrophilicity window plot. Hydrophilicity Window Size = 7; scale = Kyte-Doolittle.
 Figure 11D shows alignment between HB4 and human PTP.
 Figure 11E shows alignment between HB4 and human Reg gene.
 Figures 12A-12C show the expression of mRNA molecules corresponding to the 1-9a CNS neural thread protein cDNA sequence in neuroectodermal tumor cell lines and in rat pancreas.
 Figures 13A and 13B show mRNA transcripts corresponding to the 1-9a CNS neural thread protein cDNA sequence in human brain. This figure also demonstrates higher levels of 1-9a CNS neural thread protein-related mRNAs in AD brains compared with aged-matched controls (Figure 13A).
 Figure 13B demonstrates four different transcripts with greater abundance of the lower molecular size mRNAs in AD compared with aged controls.
 Figures 14A-14C show 1-9a Southern blot analysis of RT/PCR-derived cDNAs in neuroectodermal cell lines. A- and B-PCR amplification of 1-9a mRNA sequences in neuroectodermal cell lines, and using mRNA from newborn rat (NB) brain, AD brain, and aged control brain. Figure 14A is a longer exposure of Figure 14B. Figure 14C shows hybridization of the same blot using the 018 rat PTP probe.
 Figures 15A and 15B (SE-RT/PCR) show hybridization of the 1-9a and O18 probes with several clones isolated from SH-Sy5y cells by reverse transcribing mRNA and amplifying with primers corresponding to the known sequence of the 1-9a partial cDNA.
 Figures 16A, 16D and 16E show the partial nucleic acid sequences of the AD 2-2 cDNAs isolated from the AD brain library. Figures 16B and 16C show a hydrophilicity window plot of AD2-2 T7. Hydrophilicity Window Size = 7; scale = Kyte-Doolittle.
 Figures 16F, 16I, 16J and 16K show the partial nucleic acid sequences of the AD 3-4 cDNAs isolated from the AD brain library. Figures 16G and 16H show a hydrophilicity window plot of AD3-4. Hydrophilicity Window Size = 7; scale = Kyte-Doolittle.
 Figures 16L, 16M and 16N show the partial nucleic acid sequences of the AD 4-4 cDNAs isolated from the AD brain library.
 Figure 16O shows the partial nucleic acid sequences of the AD 16c (also called AD 10-7) cDNAs isolated from the AD brain library. Figures 16P and 16Q show a hydrophilicity window plot of AD16c-T7. Hydrophilicity Window Size = 7; scale = Kyte-Doolittle.
 Figure 16R shows the complete nucleotide sequence of the AD10-7 cDNA clone that was isolated from an AD library.
 Figure 16S shows the complete nucleotide sequence of the AD16c cDNA clone that was isolated from the AD brain library.
 Figure 17 shows alignment of partial sequences between AD 2-2 and human Reg gene.
 Figure 17A shows alignment of partial sequences between AD 2-2 and Exon 1 of Reg and rat PTP.
 Figure 17B shows alignment of partial sequences between AD 2-2 and 1-9a.
 Figure 17C shows alignment of partial sequences between AD 2-2 and AD 16c.
 Figure 18 shows alignment of partial sequences between AD 3-4 (also called AD 5-3) and the Reg gene.
 Figure 18A shows alignment of partial sequences between AD 3-4 and the 5' anchor PCR products of the 1-9a mRNA, termed WPO3-5 and 18-4.
 Figure 18B shows alignment of partial sequences between AD 3-4 and the G2a-a *EcoRI/PstI* genomic clone.
 Figure 19 shows alignment of partial sequences between AD 4-4 and AD 2-2 and 1-9a (also called SE-4 corresponding to the PCR clone which is identical to 1-9a).
 Figure 20 shows alignment of partial sequences between AD 16c and Reg gene.
 Figure 20A shows alignment of partial sequences between AD 16c and human PTP.
 Figure 20B shows alignment of partial sequences between AD 16c and AD 2-2.
 Figures 21A-21D show a genomic Southern blot analysis using the AD 3-4 as a probe; Figure 21B shows a similar

pattern of hybridization on a genomic Southern using AD 2-2 as a probe. Figures 21A-21D show a Northern blot analysis of neuroectodermal tumor cell lines using AD 3-4 as a probe. The four cell lines that exhibit AD 3-4 transcripts are neuronal in phenotype; C6 glioma cell mRNA did not hybridize with the AD 3-4 probe.

Figure 21D shows a Northern analysis of human AD and aged control brain temporal lobe tissue using the AD 3-4 probe, and demonstrates over-expression of the corresponding gene in AD (lanes labeled A) compared with aged control brains (lanes labeled C).

Figures 22, 22A, 22B, 22C, 22D, 22E, 22F, 22G and 22H show partial sequences of four genomic clones (isolated using both the 1-9a cDNA and rat PTP O-18 cDNA as probes).

Figures 23 and 23A show the alignment of the G2a-2 *Pst*I partial sequence with the Reg gene.

Figure 23B shows alignment of the G2a-2 *Pst*I-*Eco*RI sequence and the Reg gene and the rat PTP.

Figures 23C and 23D show the alignment of the G5d-1 *Pst*I sequence and the Reg gene.

Figures 24A-24D show neural thread protein expression by the 1-9a cDNA (Figure 24A) and the G2a-2 *Pst*I genomic clone (Figure 24B). Figures 24C and 24D show negative expression by the G5d-1 *Eco*RI/*Pst*I genomic clone, and pBluescript which lacks a cloned insert, respectively.

Figures 25A and 25B depict a Northern blot analysis of AD 16c mRNA in AD and aged control brains. The data shows elevated levels of AD16c mRNA expression in 6 of 9 AD compared to 1 of 6 age-matched controls.

Figure 26 depicts a Western blot analysis of AD10-7 fusion proteins using monoclonal antibodies against the expressed tag protein (T7-tag mouse monoclonal antibodies).

Figures 27A and 27B depict brightfield and darkfield microscopic analysis of the *in situ* hybridization of sense and antisense cRNA probes to human brain tissue sections of early AD.

Definitions

[0051] In the description that follows, a number of terms used in recombinant DNA technology are utilized extensively. In order to provide a clear and consistent understanding of the specification and claims, including the scope to be given such terms, the following definitions are provided.

[0052] Cloning vector. A plasmid or phage DNA or other DNA sequence which is able to replicate autonomously in a host cell, and which is characterized by one or a small number of restriction endonuclease recognition sites at which such DNA sequences may be cut in a determinable fashion without loss of an essential biological function of the vector, and into which a DNA fragment may be spliced in order to bring about its replication and cloning. The cloning vector may further contain a marker suitable for use in the identification of cells transformed with the cloning vector. Markers, for example, provide tetracycline resistance or ampicillin resistance.

[0053] Expression vector. A vector similar to a cloning vector but which is capable of enhancing the expression of a gene which has been cloned into it, after transformation into a host. The cloned gene is usually placed under the control of (i.e., operably linked to) certain control sequences such as promoter sequences. Promoter sequences may be either constitutive or inducible.

[0054] Substantially pure. As used herein means that the desired purified protein is essentially free from contaminating cellular components, said components being associated with the desired protein in nature, as evidenced by a single band following polyacrylamide-sodium dodecyl sulfate gel electrophoresis. Contaminating cellular components may include, but are not limited to, proteinaceous, carbohydrate, or lipid impurities.

[0055] The term "substantially pure" is further meant to describe a molecule which is homogeneous by one or more purity or homogeneity characteristics used by those of skill in the art. For example, a substantially pure NTP will show constant and reproducible characteristics within standard experimental deviations for parameters such as the following: molecular weight, chromatographic migration, amino acid composition, amino acid sequence, blocked or unblocked N-terminus, HPLC elution profile, biological activity, and other such parameters. The term, however, is not meant to exclude artificial or synthetic mixtures of the factor with other compounds. In addition, the term is not meant to exclude NTP fusion proteins isolated from a recombinant host.

[0056] Recombinant Host. According to the invention, a recombinant host may be any prokaryotic or eukaryotic cell which contains the desired cloned genes on an expression vector or cloning vector. This term is also meant to include those prokaryotic or eukaryotic cells that have been genetically engineered to contain the desired gene(s) in the chromosome or genome of that organism.

[0057] Recombinant vector. Any cloning vector or expression vector which contains the desired cloned gene(s).

[0058] Host. Any prokaryotic or eukaryotic cell that is the recipient of a replicable expression vector or cloning vector. A "host," as the term is used herein, also includes prokaryotic or eukaryotic cells that can be genetically engineered by well known techniques to contain desired gene(s) on its chromosome or genome. For examples of such hosts, see Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (1989).

[0059] Promoter. A DNA sequence generally described as the 5' region of a gene, located proximal to the start

codon. The transcription of an adjacent gene(s) is initiated at the promoter region. If a promoter is an inducible promoter, then the rate of transcription increases in response to an inducing agent. In contrast, the rate of transcription is not regulated by an inducing agent if the promoter is a constitutive promoter.

[0060] **Gene.** A DNA sequence that contains information needed for expressing a polypeptide or protein.

[0061] **Structural gene.** A DNA sequence that is transcribed into messenger RNA (mRNA) that is then translated into a sequence of amino acids characteristic of a specific polypeptide.

[0062] **Antisense RNA gene/Antisense RNA.** In eukaryotes, mRNA is transcribed by RNA polymerase II. However, it is also known that one may construct a gene containing a RNA polymerase II template wherein a RNA sequence is transcribed which has a sequence complementary to that of a specific mRNA but is not normally translated. Such a gene construct is herein termed an "antisense RNA gene" and such a RNA transcript is termed an "antisense RNA." Antisense RNAs are not normally translatable due to the presence of translation stop codons in the antisense RNA sequence.

[0063] **Antisense oligonucleotide.** A DNA or RNA molecule containing a nucleotide sequence which is complementary to that of a specific mRNA. An antisense oligonucleotide binds to the complementary sequence in a specific mRNA and inhibits translation of the mRNA.

[0064] **Antisense Therapy.** A method of treatment wherein antisense oligonucleotides are administered to a patient in order to inhibit the expression of the corresponding protein.

[0065] **Complementary DNA (cDNA).** A "complementary DNA," or "cDNA" gene includes recombinant genes synthesized by reverse transcription of mRNA and from which intervening sequences (introns) have been removed.

[0066] **Expression.** Expression is the process by which a polypeptide is produced from a structural gene. The process involves transcription of the gene into mRNA and the translation of such mRNA into polypeptide(s).

[0067] **Homologous/Nonhomologous** Two nucleic acid molecules are considered to be "homologous" if their nucleotide sequences share a similarity of greater than 50%, as determined by HASH-coding algorithms (Wither, W.J. and Lipman, D.J., *Proc. Natl. Acad. Sci.* 80:726-730 (1983)). Two nucleic acid molecules are considered to be "non-homologous" if their nucleotide sequences share a similarity of less than 50%.

[0068] **Ribozyme.** A ribozyme is an RNA molecule that contains a catalytic center. The term includes RNA enzymes, self-splicing RNAs, and self-cleaving RNAs.

[0069] **Ribozyme Therapy.** A method of treatment wherein ribozyme is administered to a patient in order to inhibit the translation of the target mRNA.

[0070] **Fragment.** A "fragment" of a molecule such as NTP is meant to refer to any polypeptide subset of that molecule.

[0071] **Functional Derivative.** The term "functional derivatives" is intended to include the "variants," "analogues," or "chemical derivatives" of the molecule. A "variant" of a molecule such as NTP is meant to refer to a naturally occurring molecule substantially similar to either the entire molecule, or a fragment thereof. An "analogue" of a molecule such as NTP is meant to refer to a non-natural molecule substantially similar to either the entire molecule or a fragment thereof.

[0072] A molecule is said to be "substantially similar" to another molecule if the sequence of amino acids in both molecules is substantially the same, and if both molecules possess a similar biological activity. Thus, provided that two molecules possess a similar activity, they are considered variants as that term is used herein even if one of the molecules contains additional amino acid residues not found in the other, or if the sequence of amino acid residues is not identical.

[0073] As used herein, a molecule is said to be a "chemical derivative" of another molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half-life, etc. The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, etc. Examples of moieties capable of mediating such effects are disclosed in *Remington's Pharmaceutical Sciences* (1980) and will be apparent to those of ordinary skill in the art.

[0074] **NTP.** The term "NTP" refers to a family of neural thread proteins. The NTP family includes proteins with molecular weights of about 8 kDa, 14 kDa, 17 kDa, 21 kDa, 26 kDa and 42 kDa, as described herein.

[0075] **Immuno-Polymerase Chain Reaction.** A method for the detection of antigens using specific antibody-DNA conjugates. According to this method, a linker molecule with bispecific binding affinity for DNA and antibodies is used to attach a DNA molecule specifically to an antigen-antibody complex. As a result, a specific antigen-antibody-DNA conjugate is formed. The attached DNA can be amplified by the polymerase chain reaction (PCR) using appropriate oligonucleotide primers. The presence of specific PCR products demonstrates that DNA molecules are attached specifically to antigen-antibody complexes, thus indicating the presence of antigen. (Sano *et al.*, *Science* 258:120-122 (1992)).

[0076] For example, Sano *et al.*, *supra*, constructed a streptavidin-protein A chimera that possesses specific binding affinity for biotin and immunoglobulin G. This chimera (i.e., the "linker molecule") was used to attach a biotinylated DNA specifically to antigen-monoclonal antibody complexes that had been immobilized on microtiter plate wells. A segment of the attached DNA was subsequently amplified by PCR.

Detailed Description of the Invention

[0077] This invention is directed to neural thread proteins (NTP), genetic sequences coding for an NTP mRNA or antisense mRNA, expression vectors containing the genetic sequences, recombinant hosts transformed therewith, and NTP and antisense RNA produced by such transformed recombinant host expression. This invention further relates to NTP ribozymes, and recombinant DNA molecules which code for NTP ribozymes and NTP antisense oligonucleotides. This invention further relates to antibodies directed against an NTP, as well as the use of NTP antibodies and NTP nucleic acid sequences for detection of the presence of an NTP in biological samples. The invention further relates to the use of NTP coding sequences in gene therapy.

I. Isolation of DNA Sequences Coding for Neuronal Thread Proteins

[0078] DNA sequences coding for an NTP are derived from a variety of sources. These sources include genomic DNA, cDNA, synthetic DNA, and combinations thereof.

[0079] Human NTP genomic DNA can be extracted and purified from any human cell or tissue, by means well known in the art (for example, see Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989). The NTP genomic DNA of the invention may or may not include naturally occurring introns. Moreover, such genomic DNA may be obtained in association with the 5' promoter region of the NTP gene sequences and/or with the 3' translational termination region. Further, such genomic DNA may be obtained in association with DNA sequences which encode the 5' nontranslated region of the NTP mRNA and/or with the genetic sequences which encode the 3' nontranslated region. To the extent that a host cell can recognize the transcriptional and/or translational regulatory signals associated with the expression of the mRNA and protein, then the 5' and/or 3' nontranscribed regions of the native gene, and/or, the 5' and/or 3' nontranslated regions of the mRNA, may be retained and employed for transcriptional and translational regulation.

[0080] Alternatively, an NTP mRNA can be isolated from any cell which expresses an NTP, and used to produce cDNA by means well known in the art (for example, see Sambrook *et al.*, *supra*). Preferably, the mRNA preparation used will be enriched in mRNA coding for an NTP, either naturally, by isolation from cells which produce large amounts of an NTP, or *in vitro*, by techniques commonly used to enrich mRNA preparations for specific sequences, such as sucrose gradient centrifugation, or both. An NTP mRNA may be obtained from mammalian neuronal tissue, or from cell lines derived therefrom. Preferably, human cDNA libraries are constructed from 17-18 week old fetal brain, 2 year old temporal lobe neocortex, end-stage AD cerebral cortex, or from cell lines derived from human neuronal tissue. Such cell lines may include, but are not limited to, central nervous system primitive neuroectodermal tumor cells (such as PNET1 or PNET2, as described herein), neuroblastoma cells (such as SH-Sy5y, as described herein), or human glioma cells (such as A172; ATCC CRL 1620). Alternatively, a rat cDNA library can be prepared from mRNA isolated from rat glioma cells, for example, C6 rat glioma cells (ATCC CCL107).

[0081] For cloning into a vector, suitable DNA preparations (either genomic or cDNA) are randomly sheared or enzymatically cleaved, respectively, and ligated into appropriate vectors to form a recombinant gene (either genomic or cDNA) library. A DNA sequence encoding an NTP may be inserted into a vector in accordance with conventional techniques, including blunt-ending or staggered-ending termini for ligation, restriction enzyme digestion to provide appropriate termini, filling in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and ligation with appropriate ligases. Techniques for such manipulation are disclosed by Sambrook *et al.*, *supra*, and are well known in the art.

[0082] Libraries containing NTP clones may be screened and the NTP clones identified by any means which specifically selects for NTP DNA such as, for example: 1) by hybridization with an appropriate nucleic acid probe(s) containing a sequence specific for the DNA of this protein; or, 2) by hybridization-selected translational analysis in which native mRNA hybridizes to the clone in question, is *translated in vitro*, and the translation products are further characterized; or, 3) if the cloned DNA sequences are themselves capable of expressing mRNA, by immunoprecipitation of a translated NTP product produced by the host containing the clone.

[0083] Oligonucleotide probes specific for an NTP which can be used to identify clones to this protein can be designed from knowledge of the amino acid sequence of the corresponding NTP, or homologous regions of the PTP. Alternatively, oligonucleotide probes can be designed from knowledge of the nucleotide sequence of PTP (de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990)).

[0084] The suitable oligonucleotide, or set of oligonucleotides, which is capable of encoding a fragment of the NTP gene (or which is complementary to such an oligonucleotide, or set of oligonucleotides) may be synthesized by means well known in the art (for example, see Sambrook *et al.*, *supra*). Techniques of nucleic acid hybridization and clone identification are disclosed by Sambrook *et al.*, *supra*. Those members of the above-described gene library which are found to be capable of such hybridization are then analyzed to determine the extent and nature of the NTP encoding sequences which they contain.

[0085] To facilitate the detection of the desired NTP coding sequence, the above-described DNA probe is labeled with a detectable group. Such detectable group can be any material having a detectable physical or chemical property. Such materials have been well-developed in the field of nucleic acid hybridization and in general most any label useful in such methods can be applied to the present invention. Particularly useful are radioactive labels including ^{32}P , ^3H , ^{14}C , ^{125}I , or the like. Any radioactive label may be employed which provides for an adequate signal and has sufficient half-life. The DNA probe may be labeled, for example, by nick-translation, by T4 DNA polymerase replacement synthesis, or by random priming, among other methods well known in the art (see Sambrook *et al. supra*).

[0086] Alternatively, DNA probes can be labeled with non-radioactive markers such as biotin, an enzyme, or fluorescent group.

[0087] In an alternative method of cloning NTP DNA sequences, NTP cDNAs are obtained by direct cloning of cDNAs from cell lines and brain tissue, using the 3'- and 5'-RACE methods, as described herein. Preferably, a human neuroectodermal tumor cell line or AD brain tissue is used as a source of mRNA.

II. Expressing the Gene Coding for NTP

[0088] The above-discussed methods are, therefore, capable of identifying DNA sequences which are code for an NTP or fragments thereof. In order to further characterize such DNA sequences, and in order to produce the recombinant protein, it is desirable to express the proteins which the DNA sequences encode.

[0089] To express an NTP, transcriptional and translational signals recognizable by an appropriate host are necessary. The cloned NTP DNA sequences, obtained through the methods described above, and preferably in double-stranded form, may be "operably linked" to sequences controlling transcriptional expression in an expression vector, and introduced into a host cell, either prokaryotic or eukaryotic, to produce recombinant NTP. Depending upon which strand of the NTP coding sequence is operably linked to the sequences controlling transcriptional expression, it is also possible to express an NTP antisense RNA.

[0090] Expression of the NTP in different hosts may result in different post-translational modifications which may alter the properties of the NTP. Preferably, the present invention encompasses the expression of an NTP in eukaryotic cells, and especially mammalian, insect, and yeast cells. Especially preferred eukaryotic hosts are mammalian cells. Mammalian cells provide post-translational modifications to recombinant NTP which include folding and/or phosphorylation. Most preferably, mammalian host cells include human CNS primitive neuroectodermal tumor cells, human neuroblastoma cells, human glioma cells, or rat glioma cells. Especially preferred primitive neuroectodermal tumor cells include PNET1 and PNET2, especially preferred human glioblastoma cells include Hg16 and Hg17, especially preferred human glioma cells include A 172, and especially preferred rat glioma cells include C6 (see Example 1).

[0091] Alternatively, an NTP may be expressed by prokaryotic host cells. Preferably, a recombinant NTP is expressed by such cells as a fusion protein, as described herein. An especially preferred prokaryotic host is *E. coli*. Preferred strains of *E. coli* include Y1088, Y1089, CSH18, ER1451, and ER1647 (see, for example, *Molecular Biology LabFax*, Brown, T. A., Ed., Academic Press, New York (1991)). An alternative preferred host is *Bacillus subtilis*, including such strains as BR151, YB886, MI119, MI120, and B170 (see, for example, Hardy, "Bacillus Cloning Methods," in *DNA Cloning: A Practical Approach*, IRL Press, Washington, D.C. (1985)).

[0092] A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains expression control sequences which in turn contain transcriptional regulatory information and such sequences are "operably linked" to the nucleotide sequence which encodes the protein.

[0093] Two sequences of a nucleic acid molecule are said to be operably linked when they are linked to each other in a manner which either permits both sequences to be transcribed onto the same RNA transcript, or permits an RNA transcript, begun in one sequence to be extended into the second sequence. Thus, two sequences, such as a promoter sequence and any other "second" sequence of DNA or RNA are operably linked if transcription commencing in the promoter sequence will produce an RNA transcript of the operably linked second sequence. In order to be operably linked it is not necessary that two sequences be immediately adjacent to one another.

[0094] The promoter sequences of the present invention may be either prokaryotic, eukaryotic or viral. Suitable promoters are repressible, constitutive, or inducible. Examples of suitable prokaryotic promoters include promoters capable of recognizing the T4 polymerases (Malik *et al.*, *J. Biol. Chem.* 263:1174-1181 (1984); Rosenberg *et al.*, *Gene* 59:191-200 (1987); Shinedling *et al.*, *J. Molec. Biol.* 195:471-480 (1987); Hu *et al.*, *Gene* 42:21-30 (1986)), T3, Sp6, and T7 (Chamberlin *et al.*, *Nature* 228:227-231 (1970); Bailey *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 80:2814-2818 (1983); Davanloo *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 81:2035-2039 (1984)); the P_R and P_L promoters of bacteriophage lambda (*The Bacteriophage Lambda*, Hershey, A.D., Ed., Cold Spring Harbor Press, Cold Spring Harbor, NY (1973); *Lambda II*, Hendrix, R.W., Ed., Cold Spring Harbor Press, Cold Spring Harbor, NY (1980)); the *trp*, *recA*, heat shock, and *lacZ* promoters of *E. coli*; the α -amylase (Ulmanen *et al.*, *J. Bacteriol.* 162:176-182 (1985)) and the delta-28-specific promoters of *B. subtilis* (Gilman *et al.*, *Gene* 32:11-20 (1984)); the promoters of the bacteriophages of *Bacillus* (Gryczan, In: *The Molecular Biology of the Bacilli*, Academic Press, Inc., NY (1982)); *Streptomyces* promoters (Ward *et al.*, *Mol.*

Gen. Genet. 203:468-478 (1986)); the *int* promoter of bacteriophage lambda; the *bla* promoter of the β -lactamase gene of pBR322, and the CAT promoter of the chloramphenicol acetyl transferase gene of pBR325, etc. Prokaryotic promoters are reviewed by Glick, *J. Ind. Microbiol.* 1:277-282 (1987); Cenatiempo, *Biochimie* 68:505-516 (1986); Watson *et al.*, In: *Molecular Biology of the Gene*, Fourth Edition, Benjamin Cummins, Menlo Park, CA (1987); Gottesman, *Ann. Rev. Genet.* 18:415-442 (1984); and Sambrook *et al.*, *supra*.

[0095] Preferred eukaryotic promoters include the promoter of the mouse metallothionein I gene (Hamer *et al.*, *J. Mol. Appl. Gen.* 1:273-288 (1982)); the TK promoter of Herpes virus (McKnight, *Cell* 31:355-365 (1982)); the SV40 early promoter (Benoist, *et al.*, *Nature (London)* 290:304-310 (1981)); and the yeast *gal4* gene promoter (Johnston, *et al.*, *Proc. Natl. Acad. Sci. (USA)* 79:6971-6975 (1982); Silver, *et al.*, *Proc. Natl. Acad. Sci. (USA)* 81:5951-5955 (1984)).

All of the above listed references are incorporated by reference herein.

[0096] Strong promoters are the most preferred promoters of the present invention. Examples of such preferred promoters are those which recognize the T3, SP6 and T7 polymerase promoters; the P_L promoter of bacteriophage lambda; the *recA* promoter and the promoter of the mouse metallothionein I gene. The most preferred promoter for expression in prokaryotic cells is one which is capable of recognizing the T7 polymerase promoter. The sequences of such polymerase recognition sequences are disclosed by Watson, *et al.* (In: *Molecular Biology of the Gene*, Fourth Edition, Benjamin Cummins, Menlo Park, CA, (1987)). The most preferred promoter for expression in mammalian cells is SV40 (Gorman, "High Efficiency Gene Transfer into Mammalian cells," in *DNA Cloning: A Practical Approach*, Volume II, IRL Press, Washington, D.C., pp. 143-190 (1985)).

III. Methods of Detecting NTP

[0097] This invention is directed towards methods of detecting neurological disease in a human subject, utilizing the nucleic acid probes hybridizable to NTP genes or transcripts, or antibodies specific for an NTP. By "neurological disease" is meant Alzheimer's Disease (AD), or other neurodegenerative disorders with the Alzheimer's type pathogenic changes (for example, Parkinson's disease with AD-type neurodegeneration), as well as neuroectodermal tumors, malignant astrocytomas, and glioblastomas. By "human subject" is meant any human being or any developmental form thereof, such as a human embryo or fetus, prior to birth. The diagnostic methods of the present invention do not require invasive removal of neural tissue.

[0098] The present invention additionally pertains to assays, both nucleic acid hybridization assays and immunoassays, for detecting the presence of NTP in cells or in the biological fluids of a human subject using light or electron microscopic histology, imaging, radioactive or enzyme based assays, and the like.

a. Nucleic Acid Hybridization Assays

[0099] In testing a tissue sample for an NTP using a nucleic acid hybridization assay, RNA can be isolated from tissue by sectioning on a cryostat and lysing the sections with a detergent such as SDS and a chelating agent such as EDTA, optionally with overnight digestion with proteinase K (50 μ g/ml). Such tissue is obtained by autopsy and biopsy. A preferred quantity of tissue is in the range of 1-10 milligrams. Protein is removed by phenol and chloroform extractions, and nucleic acids are precipitated with ethanol. RNA is isolated by chromatography on an oligo dT column and then eluted therefrom. Further fractionation can also be carried out, according to methods well known to those of ordinary skill in the art.

[0100] A number of techniques for molecular hybridization are used for the detection of DNA or RNA sequences in tissues; each has certain advantages and disadvantages. When large amounts of tissue are available, analysis of hybridization kinetics provides the opportunity to accurately quantitate the amount of DNA or RNA present, as well as to distinguish sequences that are closely related but not identical to the probe, and determine the percent homology.

[0101] Reactions are run under conditions of hybridization ($T_m-25^\circ\text{C}$) in which the rate of reassociation of the probe is optimal (Wetmur *et al.*, *J. Mol. Biol.* 31:349-370 (1968)). The kinetics of the reaction are second-order when the sequences in the tissue are identical to those of the probe; however, the reaction exhibits complex kinetics when probe sequences have partial homology to those in the tissue (Sharp *et al.*, *J. Mol. Biol.* 86:709-726 (1974)).

[0102] The ratio of probe to cell RNA is determined by the sensitivity desired. To detect one transcript per cell would require about 100 pg of probe per μ g of total cellular DNA or RNA. The nucleic acids are mixed, denatured, brought to the appropriate salt concentration and temperature, and allowed to hybridize for various periods of time. The rate of reassociation can be determined by quantitating the amount of probe hybridized either by hydroxyapatite chromatography (Britten *et al.*, *Science* 161:529-540 (1968)) or S1 nuclease digestion (Sutton, *Biochini. Biophys. Acta* 240: 522-531 (1971)).

[0103] A more flexible method of hybridization is the northern blot technique. This technique offers variability in the stringency of the hybridization reaction, as well as determination of the state of the retroviral sequences in the specimen under analysis. Northern analysis can be performed as described herein.

[0104] A major consideration associated with hybridization analysis of DNA or RNA sequences is the degree of relatedness the probe has with the sequences present in the specimen under study. This is important with the blotting technique, since a moderate degree of sequence homology under nonstringent conditions of hybridization can yield a strong signal even though the probe and sequences in the sample represent non-homologous genes.

[0105] The particular hybridization technique is not essential to the invention, any technique commonly used in the art being within the scope of the present invention. Typical probe technology is described in United States Patent 4,358,535 to Falkow *et al.*, incorporated by reference herein. For example, hybridization can be carried out in a solution containing 6 x SSC (10 x SSC: 1.5 M sodium chloride, 0.15 M sodium citrate, pH 7.0), 5 x Denhardt's (1 x Denhardt's: 0.2% bovine serum albumin, 0.2% polyvinylpyrrolidone, 0.02% Ficoll 400), 10 mM EDTA, 0.5 % SDS and about 10⁷ cpm of nick-translated DNA for 16 hours at 65°C.

[0106] The labeled probes, as described above, provide a general diagnostic method for detection of an NTP in tissue. The method is reasonably rapid, has a simple protocol, has reagents which can be standardized and provided as commercial kits, and allows for rapid screening of large numbers of samples.

[0107] In one method for carrying out the procedure, a clinical isolate containing RNA transcripts is fixed to a support. The affixed nucleic acid is contacted with a labeled polynucleotide having a base sequence complementary or homologous to the coding strand of the NTP gene.

[0108] The hybridization assays of the present invention are particularly well suited for preparation and commercialization in kit form, the kit comprising a carrier means compartmentalized to receive one or more container means (vial, test tube, etc.) in close confinement, each of said container means comprising one of the separate elements to be used in hybridization assay.

[0109] For example, there may be a container means containing NTP cDNA molecules suitable for labeling by "nick translation" (see, for example, Sambrook *et al.*, *supra*, for standard methodology), or labeled NTP cDNA or RNA molecules. Further container means may contain standard solutions for nick translation of NTP cDNA comprising DNA polymerase I/DNase I and unlabeled deoxyribonucleotides (i.e., dCTP, dTTP, dGTP, and dATP).

[0110] The presence of NTP RNA is determined by the variation in the appearance and/or quantity of probe-related RNA in tested tissue.

[0111] The DNA probes of this invention can also be used for differential diagnosis of hereditary or familial AD and non-hereditary or sporadic AD. The familial form of AD often occurs at an earlier age and is associated with Down's syndrome in the family. Thus, a genetic test for familial AD allows for genetic counseling of families. While much effort has been directed toward characterizing a genetic marker for familial AD (Gusella, *FASEB J* 3:2036-2041 (1989); Hooper, *J NIH Res.* 4:48-54 (1992)), genetic linkage analysis only identifies a genetic marker sequence without providing the knowledge of the function of the genomic sequence. In contrast, the cDNA probes described herein and obtained from individuals with sporadic AD encode a known protein of known function which is over-expressed in brain tissue of patients with AD.

[0112] Most cases of the AD disorder appear to be the sporadic form, although there are well-documented familial cases (Gusella, *supra*; Harrison's *Principles of Internal Medicine*, Braunwald *et al.*, Eds., Eleventh Edition, McGraw-Hill Book Company, New York, pp. 2012-2013 (1987)). A patient with familial AD, unlike a patient with sporadic AD, inherited the predisposing mutation through the germ cells. Some of the familial cases have been shown to follow an autosomal dominant pattern of inheritance (*Id.*). Thus, the DNA of a patient with familial AD will contain the inherited genetic alteration which is absent from the DNA of a patient with sporadic AD.

[0113] A method of differentiating between sporadic and familial AD in a human subject involves obtaining a biological sample from the human subject who is suspected of having Alzheimer's Disease. Then, DNA is purified from the biological sample. Finally, the DNA is contacted with a NTP DNA probe under conditions of hybridization. Familial AD is indicated by the detection of a hybrid of the probe and the DNA, whereas sporadic AD is indicated by the absence of detection of hybridization.

[0114] For example, the biological sample can be a blood sample which is subjected to differential centrifugation to enrich for white blood cells within three days of collection (Park, "PCR in the Diagnosis of Retinoblastoma," in *PCR Protocols*, Innis *et al.*, Eds., Academic Press, Inc., New York, pp. 407-415 (1990)). The DNA sample can be prepared using the sodium N-lauroylsarcosine-Proteinase K, phenol, and RNase method (Sambrook *et al.*, *supra*). DNA analysis can be performed by digesting the DNA sample, preferably 5 micrograms, with a restriction endonuclease (such as *HindIII*). Digested DNA is then fractionated using agarose gel electrophoresis, preferably, a 1 % horizontal agarose gel, for 18 hours in a buffer preferably containing 89 mM Tris-HCl (pH 8), 89 mM sodium borate and 2 mM EDTA (Gusella *et al.*, *Nature* 306:234-238 (1983)). Southern analysis can be performed using conventional techniques (Sambrook *et al.*, *supra*), and the labelled AD cDNA probes can be hybridized under conditions described above. The preferred DNA probes for this differential diagnosis method include 1-9a, AD3-4, AD4-4 and G2-2 PstI.

b. Immunoassays

[0115] Antibodies directed against an NTP can be used, as taught by the present invention, to detect and diagnose AD. Various histological staining methods, including immunohistochemical staining methods, may also be used effectively according to the teaching of the invention. Silver stain is but one method of visualizing NTP. Other staining methods useful in the present invention will be obvious to the artisan, the determination of which would not involve undue experimentation (see *generally*, for example, *A Textbook of Histology*. Eds. Bloom and Fawcett, W. B. Saunders Co., Philadelphia (1964)).

[0116] One screening method for determining whether a given compound is an NTP functional derivative comprises, for example, immunoassays employing radioimmunoassay (RIA) or enzyme-linked immunosorbent assay (ELISA) methodologies, based on the production of specific antibodies (monoclonal or polyclonal) to an NTP. For these assays, biological samples are obtained by venepuncture (blood), spinal tap (cerebral spinal fluid (CSF)), urine and other body secretions such as sweat and tears. For example, in one form of RIA, the substance under test is mixed with diluted antiserum in the presence of radiolabeled antigen. In this method, the concentration of the test substance will be inversely proportional to the amount of labeled antigen bound to the specific antibody and directly related to the amount of free labeled antigen. Other suitable screening methods will be readily apparent to those of skill in the art.

[0117] The present invention also relates to methods of detecting an NTP or functional derivatives in a sample or subject. For example, antibodies specific for an NTP, or a functional derivative, may be detectably labeled with any appropriate marker, for example, a radioisotope, an enzyme, a fluorescent label, a paramagnetic label, or a free radical.

[0118] Alternatively, antibodies specific for an NTP, or a functional derivative, may be detectably labeled with DNA by the technique of immuno-polymerase chain reaction (Sano *et al.*, *Science* 258: 120-122 (1992)). The polymerase chain reaction (PCR) procedure amplifies specific nucleic acid sequences through a series of manipulations including denaturation, annealing of oligonucleotide primers, and extension of the primers with DNA polymerase (see, for example, Mullis *et al.*, U.S. Patent No. 4,683,202; Mullis *et al.*, U.S. Patent No. 4,683,195; Loh *et al.*, *Science* 243:217 (1988)). The steps can be repeated many times, resulting in a large amplification of the number of copies of the original specific sequence. As little as a single copy of a DNA sequence can be amplified to produce hundreds of nanograms of product (Li *et al.*, *Nature* 335:414 (1988)). Other known nucleic acid amplification procedures include transcription-based amplification systems (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989); Gingeras *et al.*, WO 88/10315), and the "ligase chain reaction" in which two (or more) oligonucleotides are ligated in the presence of a nucleic acid target having the sequence of the resulting "di-oligonucleotide" thereby amplifying the di-oligonucleotide (Wu *et al.*, *Genomics* 4:560 (1989); Backman *et al.*, EP 320,308; Wallace, EP 336,731; Orgel, WO 89/09835). For example, the immuno-PCR assay can be carried out by immobilizing various amounts of the test material on the surface of microtiter wells (see Sanzo *et al.*, *supra*, page 122, footnote 7). The wells are subsequently incubated with an NTP monoclonal antibody, washed, and then incubated with biotinylated NTP DNA molecules which have been conjugated to streptavidin-protein chimera (*Id.*). This chimera binds biotin (via the streptavidin moiety) and the Fc portion of an immunoglobulin G molecule (via the protein A moiety) (*Id.*, at 120; Sanzo *et al.*, *Biol Technology* 9:1378 (1991)). The wells are then washed to remove unbound conjugates. Any NTP present in the test material will be bound by the NTP monoclonal antibody, which in turn, is bound by the protein A moiety of the biotinylated NTP DNA - streptavidin-protein A conjugate. Then, the NTP DNA sequences are amplified using PCR. Briefly, the microtiter wells are incubated with deoxyribonucleoside triphosphates, NTP oligonucleotide primers, and Taq DNA polymerase (see Sanzo *et al.*, *supra*, page 122, footnote 11). An automated thermal cycler (such as the PTC-100-96 Thermal Cycler, MJ Research, Inc.) can be used to perform PCR under standard conditions (*Id.*). The PCR products are then analyzed by agarose gel electrophoresis after staining with ethidium bromide.

[0119] Methods of making and detecting such detectably labeled antibodies or their functional derivatives are well known to those of ordinary skill in the art, and are described in more detail below. Standard reference works setting forth the general principles of immunology include the work of Klein (*Immunology: The Science of Self-Nonself Discrimination*, John Wiley & Sons, New York (1982)); Kennett *et al.* (*Monoclonal Antibodies and Hybridomas: A New Dimension in Biological Analyses*, Plenum Press, New York (1980)); Campbell ("Monoclonal Antibody Technology," In: *Laboratory Techniques in Biochemistry and Molecular Biology*, Volume 13 (Burdon, R., *et al.* eds.). Elsevier. Amsterdam (1984)); and Eisen (In: *Microbiology*, 3rd Ed. (Davis, *et al.*, Harper & Row, Philadelphia (1980)).

[0120] The term "antibody" refers both to monoclonal antibodies which are a substantially homogeneous population and to polyclonal antibodies which are heterogeneous populations. Polyclonal antibodies are derived from the sera of animals immunized with an antigen. Monoclonal antibodies (mAbs) to specific antigens may be obtained by methods known to those skilled in the art. See, for example, Kohler and Milstein, *Nature* 256:495-497 (1975) and U.S. Patent No. 4,376,110. Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof.

[0121] The monoclonal antibodies, particularly mAbs Th7, Th9, and Th10 used in the present invention, may be prepared as previously described (Gross *et al.*, *J. Clin. Invest.* 76:2115-2126 (1985); Ozturk *et al.*, *Proc. Natl. Acad.*

Sci. USA 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)). The Th monoclonal antibodies were generated against the purified pancreatic form of thread protein (*Id.*). NTP-specific polyclonal and monoclonal antibodies can also be generated against a substantially pure NTP isolated from recombinant hosts (for example, see Carroll *et al.*, "Production and Purification of Polyclonal Antibodies to the Foreign Segment of β -Galactosidase Fusion Proteins," in *DNA Cloning: A Practical Approach*, Volume III, IRL Press, Washington, D.C., pp. 89-111 (1987); Mole *et al.*, "Production of Monoclonal Antibodies Against Fusion Proteins Produced in *Escherichia coli*," in *DNA Cloning: A Practical Approach*, Volume III, IRL Press, Washington, D.C., pp. 113-1139 (1987)). Alternatively, NTP-specific polyclonal and monoclonal antibodies can be generated against a substantially pure NTP isolated from biological material such as brain tissue and cell lines, by using well known techniques.

[0122] For example, monoclonal antibodies specific for the various NTP molecules of approximately, 8, 14, 17, 21, 26 kDa and 42 kDa molecular weights may be prepared from recombinant-derived proteins, which are expressed, isolated and purified from the cDNA (i.e., 1-9a), genomic clones (G2-2 *Pst*I) and AD-NTP 3-4 cDNA clones. These NTP molecules are derived from the above cDNA's and genomic clones, inserted and produced in suitable expression vectors (see Figures 2A and 2B). Since there are regions of 60-70% homology in the 5' ends of the 1-9a NTP cDNA and PTP, one can obtain monoclonal antibodies that bind specifically to the NTP recombinant proteins and not to the pancreatic form by performing routine differential screening (See, for example, de la Monte *et al.*, *J. Clin. Invest.* 86: 1004-1013 (1990)). Although there will be monoclonal antibodies that bind to both NTP and PTP, it will be possible to generate NTP-specific monoclonal antibodies because there is a substantial sequence divergence between NTP molecules of various forms (e.g., 8, 14, 17, 21, 26 and 42 kDa) and because an epitope may be defined by as few as 6-8 amino acids.

[0123] The term "antibody" is also meant to include both intact molecules as well as fragments thereof, such as, for example, Fab and F(ab')₂, which are capable of binding antigen. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody (Wahl *et al.*, *J. Nucl. Med.* 24:316-325 (1983)).

[0124] It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies useful in the present invention may be used for the detection and quantitation of an NTP according to the methods disclosed herein in order to detect and diagnose AD in the same manner as an intact antibody. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments).

[0125] An antibody is said to be "capable of binding" a molecule if it is capable of specifically reacting with the molecule to thereby bind the molecule to the antibody. The term "epitope" is meant to refer to that portion of any molecule capable of being bound by an antibody which can also be recognized by that antibody. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and have specific three dimensional structural characteristics as well as specific charge characteristics.

[0126] An "antigen" is a molecule capable of being bound by an antibody which is additionally capable of inducing an animal to produce antibody capable of binding to an epitope of that antigen. An antigen may have one, or more than one epitope. The specific reaction referred to above is meant to indicate that the antigen will react, in a highly selective manner, with its corresponding antibody and not with the multitude of other antibodies which may be evoked by other antigens.

[0127] The antibodies, or fragments of antibodies, useful in the present invention may be used to quantitatively or qualitatively detect the presence of cells which contain the NTP antigens. Thus, the antibodies (or fragments thereof) useful in the present invention may be employed histologically to detect or visualize the presence of an NTP.

[0128] Such an assay for an NTP typically comprises incubating a biological sample from said subject suspected of having such a condition in the presence of a detectably labeled binding molecule (e.g., antibody) capable of identifying an NTP, and detecting said binding molecule which is bound in a sample.

[0129] Thus, in this aspect of the invention, a biological sample may be treated with nitrocellulose, or other solid support which is capable of immobilizing cells, cell particles or soluble proteins. The support may then be washed with suitable buffers followed by treatment with the detectably labeled NTP-specific antibody. The solid phase support may then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on said solid support may then be detected by conventional means.

[0130] By "solid phase support" is intended any support capable of binding antigen or antibodies. Well-known supports, or carriers, include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads. Those skilled in the art will note many other suitable carriers for binding monoclonal antibody or

antigen, or will be able to ascertain the same by use of routine experimentation.

[0131] One embodiment for carrying out the diagnostic assay of the present invention on a biological sample containing an NTP, comprises:

- (a) contacting a detectably labeled NTP-specific antibody with a solid support to effect immobilization of said NTP-specific antibody or a fragment thereof;
- (b) contacting a sample suspected of containing an NTP with said solid support;
- (c) incubating said detectably labeled NTP-specific antibody with said support for a time sufficient to allow the immobilized NTP-specific antibody to bind to the NTP;
- (d) separating the solid phase support from the incubation mixture obtained in step (c); and
- (e) detecting the bound label and thereby detecting and quantifying NTP.

[0132] Alternatively, labeled NTP-specific antibody/NTP complexes in a sample may be separated from a reaction mixture by contacting the complex with an immobilized antibody or protein which is specific for an immunoglobulin, e.g., *Staphylococcus* protein A, *Staphylococcus* protein G, anti-IgM or anti-IgG antibodies. Such anti-immunoglobulin antibodies may be polyclonal, but are preferably monoclonal. The solid support may then be washed with a suitable buffer to give an immobilized NTP/labeled NTP-specific antibody complex. The label may then be detected to give a measure of an NTP.

[0133] This aspect of the invention relates to a method for detecting an NTP or a fragment thereof in a sample comprising:

- (a) contacting a sample suspected of containing an NTP with an NTP-specific antibody or fragment thereof which binds to NTP; and
- (b) detecting whether a complex is formed.

The invention also relates to a method of detecting an NTP in a sample, further comprising:

- (c) contacting the mixture obtained in step (a) with an Fc binding molecule, such as an antibody, *Staphylococcus* protein A, or *Staphylococcus* protein G, which is immobilized on a solid phase support and is specific for the NTP-specific antibody to give a NTP/NTP-specific antibody immobilized antibody complex;
- (d) washing the solid phase support obtained in step (c) to remove unbound NTP/NTP-specific antibody complex;
- (e) and detecting the label bound to said solid support.

[0134] Of course, the specific concentrations of detectably labeled antibody and NTP, the temperature and time of incubation, as well as other assay conditions may be varied, depending on various factors including the concentration of an NTP in the sample, the nature of the sample, and the like. The binding activity of a given lot of anti-NTP antibody may be determined according to well known methods. Those skilled in the art will be able to determine operative and optimal assay conditions for each determination by employing routine experimentation.

[0135] Other such steps as washing, stirring, shaking, filtering and the like may be added to the assays as is customary or necessary for the particular situation.

[0136] One of the ways in which the NTP-specific antibody can be detectably labeled is by linking the same to an enzyme. This enzyme, in turn, when later exposed to its substrate, will react with the substrate in such a manner as to produce a chemical moiety which can be detected, for example, by spectrophotometric, fluorometric or by visual means. Enzymes which can be used to detectably label the NTP-specific antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-V-steroid isomerase, yeast alcohol dehydrogenase, α -glycerophosphate dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, β -galactosidase, ribonuclease, urease, catalase, glucose-VI-phosphate dehydrogenase, glucoamylase and acetylcholinesterase.

[0137] Detection may be accomplished using any of a variety of immunoassays. For example, by radioactively labeling the NTP-specific antibodies or antibody fragments, it is possible to detect NTP through the use of radioimmune assays. A good description of a radioimmune assay may be found in *Laboratory Techniques and Biochemistry in Molecular Biology*, by Work, et al., North Holland Publishing Company, NY (1978), with particular reference to the chapter entitled "An introduction to Radioimmune Assay and Related Techniques" by Chard, incorporated by reference herein.

[0138] The radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or by autoradiography. Isotopes which are particularly useful for the purpose of the present invention are: ^3H , ^{125}I , ^{131}I , ^{35}S , ^{14}C , and preferably ^{125}I .

[0139] It is also possible to label the NTP-specific antibody with a fluorescent compound. When the fluorescently labeled antibody is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labelling compounds are fluorescein isothiocyanate, rhodamine, phyco-

erytherin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

[0140] The NTP-specific antibody can also be detectably labeled using fluorescence emitting metals such as ^{152}Eu , or others of the lanthanide series. These metals can be attached to the NTP-specific antibody using such metal chelating groups as diethylenetriaminepentaacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA).

[0141] The NTP-specific antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent tagged NTP-specific antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, thionin, acridinium ester, imidazole, acridinium salt and oxalate ester.

[0142] The NTP-specific antibody may also be labeled with biotin and then reacted with avidin. A biotin-labeled DNA fragment will be linked to the NTP-biotinylated monoclonal antibody by an avidin bridge. NTP molecules are then detected by polymerase chain reaction (PCR) amplification of the DNA fragment with specific primers (Sano *et al.*, *Science* 258: 120-122 (1992)).

[0143] Likewise, a bioluminescent compound may be used to label the NTP-specific antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

[0144] Detection of the NTP-specific antibody may be accomplished by a scintillation counter, for example, if the detectable label is a radioactive gamma emitter, or by a fluorometer, for example, if the label is a fluorescent material. In the case of an enzyme label, the detection can be accomplished by colorimetric methods which employ a substrate for the enzyme. Detection may also be accomplished by visual comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

[0145] The detection of foci of such detectably labeled antibodies is indicative of a disease or dysfunctional state as previously described. For the purposes of the present invention, the NTP which is detected by this assay may be present in a biological sample. Any sample containing an NTP can be used. However, one of the benefits of the present diagnostic invention is that invasive tissue removal may be avoided. Therefore, preferably, the sample is a biological solution such as, for example, cerebrospinal fluid, amniotic fluid, blood, serum, urine and the like. However, the invention is not limited to assays using only these samples, it being possible for one of ordinary skill in the art to determine suitable conditions which allow the use of other samples.

[0146] For example, the three-site monoclonal antibody-based immunoradiometric assays (M-IRMA) may be used to measure NTP levels in a biological fluid, such as CSF. It is possible to obtain, by spinal tap, on a routine basis, CSF from individuals suspected of having AD. Thus, the diagnosis of AD can be established by a simple, non-invasive immunoassay which reveals NTP levels greatly increased over normal levels.

[0147] In one embodiment, as described above, this examination for AD is accomplished by removing samples of biological fluid and incubating such samples in the presence of detectably labeled antibodies (or antibody fragments). In a preferred embodiment, this technique is accomplished in a non-invasive manner through the use of magnetic imaging, fluorography, etc.

[0148] Preferably, the detection of cells which express an NTP may be accomplished by *in vivo* imaging techniques, in which the labeled antibodies (or fragments thereof) are provided to a subject, and the presence of the NTP is detected without the prior removal of any tissue sample. Such *in vivo* detection procedures have the advantage of being less invasive than other detection methods, and are, moreover, capable of detecting the presence of NTP in tissue which cannot be easily removed from the patient, such as brain tissue.

[0149] Using *in vivo* imaging techniques, it will be possible to differentiate between AD and a brain tumor because NTP will be detected throughout the brain in an AD patient, while NTP will be localized in discrete deposits in the case of brain tumors. For example, in brains of AD patients, NTP will be found in the temporal, parietal and frontal cortices as well as the amygdala and hippocampus. Favored sites for astrocytomas include the cerebrum, cerebellum, thalamus, optic chiasma, and pons (*Harrison's Principles of Internal Medicine*, Petersdorf *et al.*, Eds., Tenth Edition. McGraw-Hill Book Company, New York, p.2076 (1983)), and glioblastoma multiforme is predominantly cerebral in location (*Id.* at 2075).

[0150] There are many different *in vivo* labels and methods of labeling known to those of ordinary skill in the art. Examples of the types of labels which can be used in the present invention include radioactive isotopes and paramagnetic isotopes. Those of ordinary skill in the art will know of other suitable labels for binding to the antibodies used in the invention, or will be able to ascertain such, using routine experimentation. Furthermore, the binding of these labels to the antibodies can be done using standard techniques common to those of ordinary skill in the art.

[0151] An important factor in selecting a radionuclide for *in vivo* diagnosis is that the half-life of a radionuclide be long enough so that it is still detectable at the time of maximum uptake by the target, but short enough so that deleterious radiation upon the host is minimized. Ideally, a radionuclide used for *in vivo* imaging will lack a particulate emission, but produce a large number of photons in the 140-200 keV range, which maybe readily detected by conventional

gamma cameras.

[0152] For *in vivo* diagnosis radionuclides may be bound to antibody either directly or indirectly by using an intermediary functional group. Intermediary functional groups which are often used in binding radioisotopes which exist as metallic ions to immunoglobulins are DTPA and EDTA. Typical examples of ions which can be bound to immunoglobulins are ^{99m}Tc , ^{123}I , ^{111}In , ^{131}I , ^{97}Ru , ^{67}Cu , ^{67}Ga , ^{125}I , ^{68}Ga , ^{72}As , ^{89}Zr , and ^{201}Tl .

[0153] For diagnostic *in vivo* imaging, the type of detection instrument available is a major factor in selecting a given radionuclide. The radionuclide chosen must have a type of decay which is detectable for a given type of instrument. In general, any conventional method for visualizing diagnostic imaging can be utilized in accordance with this invention. For example, PET, gamma, beta, and MRI detectors can be used to visualize diagnostic imaging.

[0154] The antibodies useful in the invention can also be labeled with paramagnetic isotopes for purposes of *in vivo* diagnosis. Elements which are particularly useful, as in Magnetic Resonance Imaging (MRI), include ^{157}Gd , ^{55}Mn , ^{162}Dy , and ^{56}Fe .

[0155] The antibodies (or fragments thereof) useful in the present invention are also particularly suited for use in *in vitro* immunoassays to detect the presence of an NTP in body tissue, fluids (such as CSF), or cellular extracts. In such immunoassays, the antibodies (or antibody fragments) may be utilized in liquid phase or, preferably, bound to a solid-phase carrier, as described above.

[0156] Those of ordinary skill in the art will know of other suitable labels which may be employed in accordance with the present invention. The binding of these labels to antibodies or fragments thereof can be accomplished using standard techniques commonly known to those of ordinary skill in the art. Typical techniques are described by Kennedy, *et al.* (*Clin. Chim. Acta* 70:1-31 (1976)) and Schurs, *et al.* (*Clin. Chim. Acta* 81:1-40 (1977)). Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimido-benzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

[0157] *In situ* detection may be accomplished by removing a histological specimen from a patient, and providing the combination of labeled antibodies of the present invention to such a specimen. The antibody (or fragment) is preferably provided by applying or by overlaying the labeled antibody (or fragment) to a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of an NTP, but also the distribution of an NTP on the examined tissue. Using the present invention, those of ordinary skill will readily perceive that any of a wide variety of histological methods (such as staining procedures) can be modified in order to achieve such *in situ* detection.

[0158] The binding molecules of the present invention may be adapted for utilization in an immunometric assay, also known as a "two-site" or "sandwich" assay. In a typical immunometric assay, a quantity of unlabeled antibody (or fragment of antibody) is bound to a solid support that is insoluble in the fluid being tested (i.e., CSF) and a quantity of detectably labeled soluble antibody is added to permit detection and/or quantitation of the ternary complex formed between solid-phase antibody, antigen, and labeled antibody.

[0159] Typical, and preferred, immunometric assays include "forward" assays in which the antibody bound to the solid phase is first contacted with the sample being tested to extract the antigen from the sample by formation of a binary solid phase antibody-antigen complex. After a suitable incubation period, the solid support is washed to remove the residue of the fluid sample, including unreacted antigen, if any, and then contacted with the solution containing an unknown quantity of labeled antibody (which functions as a "reporter molecule"). After a second incubation period to permit the labeled antibody to complex with the antigen bound to the solid support through the unlabeled antibody, the solid support is washed a second time to remove the unreacted labeled antibody. This type of forward sandwich assay may be a simple "yes/no" assay to determine whether antigen is present or may be made quantitative by comparing the measure of labeled antibody with that obtained for a standard sample containing known quantities of antigen. Such "two-site" or "sandwich" assays are described by Wide at pages 199-206 of *Radioimmune Assay Method*, edited by Kirkham and Hunter, E. & S. Livingstone, Edinburgh, 1970.

[0160] In another type of "sandwich" assay, which may also be useful with the antigens of the present invention, the so-called "simultaneous" and "reverse" assays are used. A simultaneous assay involves a single incubation step as the antibody bound to the solid support and labeled antibody are both added to the sample being tested at the same time. After the incubation is completed, the solid support is washed to remove the residue of fluid sample and uncomplexed labeled antibody. The presence of labeled antibody associated with the solid support is then determined as it would be in a conventional "forward" sandwich assay.

[0161] In the "reverse" assay, stepwise addition first of a solution of labeled antibody to the fluid sample followed by the addition of unlabeled antibody bound to a solid support after a suitable incubation period is utilized. After a second incubation, the solid phase is washed in conventional fashion to free it of the residue of the sample being tested and the solution of unreacted labeled antibody. The determination of labeled antibody associated with a solid support is then determined as in the "simultaneous" and "forward" assays.

[0162] The above-described *in vitro* or *in vivo* detection methods may be used in the detection and diagnosis of AD without the necessity of removing tissue. Such detection methods may be used to assist in the determination of the stage of neurological deterioration in AD by evaluating and comparing the concentration of an NTP in the biological

sample.

[0163] As used herein, an effective amount of a diagnostic reagent (such as an antibody or antibody fragment) is one capable of achieving the desired diagnostic discrimination and will vary depending on such factors as age, condition, sex, the extent of disease of the subject, counterindications, if any, and other variables to be adjusted by the physician. The amount of such materials which are typically used in a diagnostic test are generally between 0.1 to 5 mg, and preferably between 0.1 to 0.5 mg.

[0164] The assay of the present invention is also ideally suited for the preparation of a kit. Such a kit may comprise a carrier means being compartmentalized to receive in close confinement therewith one or more container means such as vials, tubes and the like, each of said container means comprising the separate elements of the immunoassay.

[0165] For example, there may be a container means containing a first antibody immobilized on a solid phase support, and a further container means containing a second detectably labeled antibody in solution. Further container means may contain standard solutions comprising serial dilutions of the NTP to be detected. The standard solutions of an NTP may be used to prepare a standard curve with the concentration of NTP plotted on the abscissa and the detection signal on the ordinate. The results obtained from a sample containing an NTP may be interpolated from such a plot to give the concentration of the NTP.

IV. Isolation of NTP

[0166] The NTP proteins or fragments of this invention may be obtained by expression from recombinant DNA as described above. Alternatively, an NTP may be purified from biological material.

[0167] For purposes of the present invention, one method of purification which is illustrative, without being limiting, consists of the following steps.

[0168] A first step in the purification of an NTP includes extraction of the NTP fraction from a biological sample, such as brain tissue or CSF, in buffers, with or without solubilizing agents such as urea, formic acid, detergent, or thiocyanate.

[0169] A second step includes subjecting the solubilized material to ion-exchange chromatography on Mono-Q or Mono-S columns (Pharmacia LKB Biotechnology, Inc; Piscataway, NJ). Similarly, the solubilized material may be separated by any other process wherein molecules can be separated according to charge density, charge distribution and molecular size, for example. Elution of the NTP from the ion-exchange resin are monitored by an immunoassay, such as M-IRMA, on each fraction. Immunoreactive peaks would be then dialyzed, lyophilized, and subjected to molecular sieve, or gel chromatography.

[0170] Molecular sieve or gel chromatography is a type of partition chromatography in which separation is based on molecular size. Dextran, polyacrylamide, and agarose gels are commonly used for this type of separation. One useful gel for the present invention is Sepharose 12 (Pharmacia LKB Biotechnology, Inc.). However, other methods, known to those of skill in the art may be used to effectively separate molecules based on size.

[0171] A fourth step in a purification protocol for an NTP includes analyzing the immunoreactive peaks by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), a further gel chromatographic purification step, and staining, such as, for example, silver staining.

[0172] A fifth step in a purification method includes subjecting the NTP obtained after SDS-PAGE to affinity chromatography, or any other procedure based upon affinity between a substance to be isolated and a molecule to which it can specifically bind. For further purification of an NTP, affinity chromatography on Sepharose conjugated to anti-NTP mAbs (such as Th9, or specific mAbs generated against substantially pure NTP) can be used. Alternative methods, such as reverse-phase HPLC, or any other method characterized by rapid separation with good peak resolution are useful.

[0173] Another method to purify an NTP is to use concentrated CSF obtained from patients with AD. For this procedure, 30-40 milliliters are concentrated by lyophilization or Amicon filtration or the like, and subjected to two dimensional gel electrophoresis. Proteins are separated in one direction by charge in a pH gradient and then, subjected to molecular sieve chromatography in the other direction by polyacrylamide gel electrophoresis. NTP-immunoreactive proteins are identified as spots by the Th monoclonal antibodies (for example, Th 9) using Western blot analysis. The gel is cut and NTP proteins are eluted from the gel. NTP purified in this manner can be sequenced or used to make new monoclonal antibodies.

[0174] It will be appreciated that other purification steps may be substituted for the preferred method described above. Those of skill in the art will be able to devise alternate purification schemes without undue experimentation.

V. Gene Therapy Using Antisense Oligonucleotides and Ribozymes

[0175] Antisense oligonucleotides have been described as naturally occurring biological inhibitors of gene expression in both prokaryotes (Mizuno *et al.*, *Proc. Natl. Acad. Sci. USA* 81:1966-1970 (1984)) and eukaryotes (Heywood, *Nucleic Acids Res.* 14:6771-6772 (1986)), and these sequences presumably function by hybridizing to complementary mRNA

sequences, resulting in hybridization arrest of translation (Paterson, *et al.*, *Proc. Natl. Acad. Sci. USA*, 74:4370-4374 (1987)).

[0176] Antisense oligonucleotides are short synthetic DNA or RNA nucleotide molecules formulated to be complementary to a specific gene or RNA message. Through the binding of these oligomers to a target DNA or mRNA sequence, transcription or translation of the gene can be selectively blocked and the disease process generated by that gene can be halted (see, for example, Jack Cohen, *Oligodeoxynucleotides, Antisense Inhibitors of Gene Expression*, CRC Press (1989)). The cytoplasmic location of mRNA provides a target considered to be readily accessible to antisense oligodeoxynucleotides entering the cell; hence much of the work in the field has focused on RNA as a target. Currently, the use of antisense oligodeoxynucleotides provides a useful tool for exploring regulation of gene expression *in vitro* and in tissue culture (Rothenberg, *et al.*, *J. Natl. Cancer Inst.* 81:1539-1544 (1989)).

[0177] Antisense therapy is the administration of exogenous oligonucleotides which bind to a target polynucleotide located within the cells. For example, antisense oligonucleotides may be administered systemically for anticancer therapy (Smith, International Application Publication No. WO 90/09180). As described herein, NTP-related proteins are produced by neuroectodermal tumor cells, malignant astrocytoma cells, glioblastoma cells, and in relatively high concentrations (i.e., relative to controls) in brain tissue of AD patients. Thus, NTP antisense oligonucleotides of the present invention may be active in treatment against AD, as well as neuroectodermal tumors, malignant astrocytomas, and glioblastomas.

[0178] The NTP antisense oligonucleotides of the present invention include derivatives such as S-oligonucleotides (phosphorothioate derivatives or S-oligos, see Jack Cohen, *supra*). S-oligos (nucleoside phosphorothioates) are isoelectronic analogs of an oligonucleotide (O-oligo) in which a nonbridging oxygen atom of the phosphate group is replaced by a sulfur atom. The S-oligos of the present invention may be prepared by treatment of the corresponding O-oligos with 3*H*-1,2-benzodithiol-3-one-1,1-dioxide which is a sulfur transfer reagent. See Iyer *et al.*, *J. Org. Chem.* 55: 4693-4698 (1990); and Iyer *et al.*, *J. Am. Chem. Soc.* 112:1253-1254 (1990), the disclosures of which are fully incorporated by reference herein.

[0179] As described herein, sequence analysis of an NTP cDNA clone shows that NTP contains sequences which are nonhomologous to PTP DNA sequences (see Figure 9). Thus, the NTP antisense oligonucleotides of the present invention may be RNA or DNA which is complementary to and stably hybridizes with such sequences which are specific for an NTP. Use of an oligonucleotide complementary to this region allows for the selective hybridization to NTP mRNA and not to mRNA specifying PTP. Preferably, the NTP antisense oligonucleotides of the present invention are a 15 to 30-mer fragment of the antisense DNA molecule coding for the nonhomologous sequences of the AD 3-4 cDNA, such as:

1. 5'-CCGATTCCAACAGACCATCAT-3' [SEQ ID NO: 1];
2. 5'-CCAACAGACCATCATTCACC-3' [SEQ ID NO: 2]; and
3. 5'-CCAAACCGATTCCAACAGACC-3' [SEQ ID NO: 3].

[0180] Preferred antisense oligonucleotides bind to the 5'-end of the AD10-7 mRNA. Such antisense oligonucleotides may be used to down regulate or inhibit expression of the NTP gene. Examples of such antisense oligonucleotides (30-mers) include:

1. 5'-CCTGGGCAACAAGAGCGAAAACCTCCATCTC-3' [SEQ ID NO: 4];
2. 5'-ATCGCTTGAACCCGGGAGGCGGAGGTTGCG-3' [SEQ ID NO: 5]; and
3. 5'-GGGGAGGCTGAGGCAGGAGAATCGCTTGAA-3' [SEQ ID NO: 6].

[0181] Included as well in the present invention are pharmaceutical compositions comprising an effective amount of at least one of the NTP antisense oligonucleotides of the invention in combination with a pharmaceutically acceptable

carrier. In one embodiment, a single NTP antisense oligonucleotide is utilized. In another embodiment, two NTP antisense oligonucleotides are utilized which are complementary to adjacent regions of the NTP genome. Administration of two NTP antisense oligonucleotides which are complementary to adjacent regions of the genome or corresponding mRNA may allow for more efficient inhibition of NTP genomic transcription or mRNA translation, resulting in more effective inhibition of NTP production.

[0182] Preferably, the NTP antisense oligonucleotide is coadministered with an agent which enhances the uptake of the antisense molecule by the cells. For example, the NTP antisense oligonucleotide may be combined with a lipophilic cationic compound which may be in the form of liposomes. The use of liposomes to introduce nucleotides into cells is taught, for example, in U.S. Patent Nos. 4,897,355 and 4,394,448, the disclosures of which are incorporated by reference in their entirety. See also U.S. Patent Nos. 4,235,871, 4,231,877, 4,224,179, 4,753,788, 4,673,567, 4,247,411, 4,814,270 for general methods of preparing liposomes comprising biological materials.

[0183] Alternatively, the NTP antisense oligonucleotide may be combined with a lipophilic carrier such as any one of a number of sterols including cholesterol, cholate and deoxycholic acid. A preferred sterol is cholesterol.

[0184] In addition, the NTP antisense oligonucleotide may be conjugated to a peptide that is ingested by cells. Examples of useful peptides include peptide hormones, antigens or antibodies, and peptide toxins. By choosing a peptide that is selectively taken up by the neoplastic cells, specific delivery of the antisense agent may be effected. The NTP antisense oligonucleotide may be covalently bound via the 5'OH group by formation of an activated aminoalkyl derivative. The peptide of choice may then be covalently attached to the activated NTP antisense oligonucleotide via an amino and sulfhydryl reactive hetero bifunctional reagent. The latter is bound to a cysteine residue present in the peptide. Upon exposure of cells to the NTP antisense oligonucleotide bound to the peptide, the peptidyl antisense agent is endocytosed and the NTP antisense oligonucleotide binds to the target NTP mRNA to inhibit translation (Haralambid *et al.*, WO 8903849; Lebleu *et al.*, EP 0263740).

[0185] The NTP antisense oligonucleotides and the pharmaceutical compositions of the present invention may be administered by any means that achieve their intended purpose. For example, administration may be by parenteral, subcutaneous, intravenous, intramuscular, intra-peritoneal, or transdermal routes. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired.

[0186] Compositions within the scope of this invention include all compositions wherein the NTP antisense oligonucleotide is contained in an amount effective to achieve inhibition of proliferation and/or stimulate differentiation of the subject cancer cells, or alleviate AD. While individual needs vary, determination of optimal ranges of effective amounts of each component is with the skill of the art. Typically, the NTP antisense oligonucleotide may be administered to mammals, e.g. humans, at a dose of 0.005 to 1 mg/kg/day, or an equivalent amount of the pharmaceutically acceptable salt thereof, per day of the body weight of the mammal being treated.

[0187] Alternatively, antisense oligonucleotides can be prepared which are designed to interfere with transcription of the NTP gene by binding transcribed regions of duplex DNA (including introns, exons, or both) and forming triple helices (Froehler *et al.*, WO 91/06626; Toole, WO 92/10590). Preferred oligonucleotides for triple helix formation are oligonucleotides which have inverted polarities for at least two regions of the oligonucleotide (Id.). Such oligonucleotides comprise tandem sequences of opposite polarity such as 3'---5'-L-5'---3', or 5'---3'-L-3'---5', wherein L represents a 0-10 base oligonucleotide linkage between oligonucleotides. The inverted polarity form stabilizes single-stranded oligonucleotides to exonuclease degradation (Froehler *et al.*, *supra*). Preferred triple helix-forming oligonucleotides are based upon SEQ ID NOs 1-3:

1. 3'-TACTACCAGACAACCTTAGCC-5'-L-
5'-CCGATTCCAACAGACCATCAT-3' [SEQ ID NO: 7];
2. 5'-CCGATTCCAACAGACCATCAT-3'-L-
3'-TACTACCAGACAACCTTAGCC-5' [SEQ ID NO: 8];
3. 3'-CCACCTTACTACCAGACAACC-5'-L-
5'-CCAACAGACCATCATTCCACC-3' [SEQ ID NO: 9];
4. 5'-CCAACAGACCATCATTCCACC-3'-L-
3'-CCACCTTACTACCAGACAACC-5' [SEQ ID NO: 10];
5. 3'-CCAGACAACCTTAGCCAAACC-5'-L-
5'-CCAAACCGATTCCAACAGACC-3' [SEQ ID NO: 11]; and
6. 5'-CCAAACCGATTCCAACAGACC-3'-L-
3'-CCAGACAACCTTAGCCAAACC-5' [SEQ ID NO: 12].

and Thus, triple helix-forming oligonucleotides 1 and 2 are represented as 3'[SEQ ID NO: 1]5'-L-5'[SEQ ID NO: 1]3' and 5'[SEQ ID NO: 1]3'-L-3'[SEQ ID NO: 1]5', respectively. Triple helix-forming oligonucleotides 3 and 4 are represented as 3'[SEQ ID NO: 2]5'-L-5'[SEQ ID NO: 2]3' and 5'[SEQ ID NO: 2]3'-L-3'[SEQ ID NO: 2]5', respectively. Triple helix-forming oligonucleotides 5 and 6 are represented as 3'[SEQ ID NO: 3]5'-L-5'[SEQ ID NO: 3]3' and 5'[SEQ ID NO: 3]3'-L-3'[SEQ ID NO: 3]5', respectively. Of course, similar triple helix-forming oligonucleotide may be prepared with SEQ ID NOs. 4-6, or fragments thereof.

[0188] In therapeutic application, the triple helix-forming oligonucleotides can be formulated in pharmaceutical preparations for a variety of modes of administration, including systemic or localized administration, as described above.

[0189] The antisense oligonucleotides of the present invention may be prepared according to any of the methods that are well known to those of ordinary skill in the art, as described above.

[0190] Ribozymes provide an alternative method to inhibit mRNA function. Ribozymes may be RNA enzymes, self-splicing RNAs, and self-cleaving RNAs (Cech *et al.*, *Journal of Biological Chemistry* 267:17479-17482 (1992)). It is possible to construct *de novo* ribozymes which have an endonuclease activity directed in *trans* to a certain target sequence. Since these ribozymes can act on various sequences, ribozymes can be designed for virtually any RNA substrate. Thus, ribozymes are very flexible tools for inhibiting the expression of specific genes and provide an alternative to antisense constructs.

[0191] A ribozyme against chloramphenicol acetyltransferase mRNA has been successfully constructed (Haseloff *et al.*, *Nature* 334:585-591 (1988); Uhlenbeck *et al.*, *Nature* 328:596-600 (1987)). The ribozyme contains three structural domains: 1) a highly conserved region of nucleotides which flank the cleavage site in the 5' direction; 2) the highly conserved sequences contained in naturally occurring cleavage domains of ribozymes, forming a base-paired stem; and 3) the regions which flank the cleavage site on both sides and ensure the exact arrangement of the ribozyme in relation to the cleavage site and the cohesion of the substrate and enzyme. RNA enzymes constructed according to this model have already proved suitable *in vitro* for the specific cleaving of RNA sequences (Haseloff *et al.*, *supra*).

[0192] Alternatively, hairpin ribozymes may be used in which the active site is derived from the minus strand of the satellite RNA of tobacco ring spot virus (Hampel *et al.*, *Biochemistry* 28:4929-4933 (1989)). Recently, a hairpin ribozyme was designed which cleaves human immunodeficiency virus type 1 RNA (Ojwang *et al.*, *Proc. Natl. Acad. Sci. USA* 89:10802-10806 (1992)). Other self-cleaving RNA activities are associated with hepatitis delta virus (Kuo *et al.*, *J. Virol.* 62:4429-4444 (1988)).

[0193] As discussed above, preferred targets for NTP ribozymes are the nucleotide sequences which are not homologous with PTP sequences. Preferably, the NTP ribozyme molecule of the present invention is designed based upon the chloramphenicol acetyltransferase ribozyme or hairpin ribozymes, described above. Alternatively, NTP ribozyme molecules are designed as described by Eckstein *et al.* (International Publication No. WO 92/07065) who disclose catalytically active ribozyme constructions which have increased stability against chemical and enzymatic degradation, and thus are useful as therapeutic agents.

[0194] In an alternative approach, an external guide sequence (EGS) can be constructed for directing the endogenous ribozyme, RNase P, to intracellular NTP mRNA, which is subsequently cleaved by the cellular ribozyme (Altman *et al.*, U.S. Patent No. 5,168,053). Preferably, the NTP EGS comprises a ten to fifteen nucleotide sequence complementary to an NTP mRNA and a 3'-NCCA nucleotide sequence, wherein N is preferably a purine (*Id.*). After NTP EGS molecules are delivered to cells, as described below, the molecules bind to the targeted NTP mRNA species by forming base pairs between the NTP mRNA and the complementary NTP EGS sequences, thus promoting cleavage of NTP mRNA by RNase P at the nucleotide at the 5' side of the base-paired region (*Id.*).

[0195] Included as well in the present invention are pharmaceutical compositions comprising an effective amount of at least one NTP ribozyme or NTP EGS of the invention in combination with a pharmaceutically acceptable carrier. Preferably, the NTP ribozyme or NTP EGS is coadministered with an agent which enhances the uptake of the ribozyme or NTP EGS molecule by the cells. For example, the NTP ribozyme or NTP EGS may be combined with a lipophilic cationic compound which may be in the form of liposomes, as described above. Alternatively, the NTP ribozyme or NTP EGS may be combined with a lipophilic carrier such as any one of a number of sterols including cholesterol, cholate and deoxycholic acid. A preferred sterol is cholesterol.

[0196] The NTP ribozyme or NTP EGS, and the pharmaceutical compositions of the present invention may be administered by any means that achieve their intended purpose. For example, administration may be by parenteral, subcutaneous, intravenous, intramuscular, intra-peritoneal, or transdermal routes. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired. For example, as much as 700 milligrams of antisense oligodeoxynucleotide has been administered intravenously to a patient over a course of 10 days (i.e., 0.05 mg/kg/hour) without signs of toxicity (Sterling, "Systemic Antisense Treatment Reported," *Genetic Engineering News* 12(12):1, 28 (1992)).

[0197] Compositions within the scope of this invention include all compositions wherein the NTP ribozyme or NTP EGS is contained in an amount which is effective to achieve inhibition of proliferation and/or stimulate differentiation of the subject cancer cells, or alleviate AD. While individual needs vary, determination of optimal ranges of effective amounts of each component is with the skill of the art.

[0198] In addition to administering the NTP antisense oligonucleotides, ribozymes, or NTP EGS as a raw chemical in solution, the therapeutic molecules may be administered as part of a pharmaceutical preparation containing suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the NTP antisense oligonucleotide, ribozyme, or NTP EGS into preparations which can be used pharmaceutically.

[0199] Suitable formulations for parenteral administration include aqueous solutions of the NTP antisense oligonucleotides, ribozymes, NTP EGS in water-soluble form, for example, water-soluble salts. In addition, suspensions of the active compounds as appropriate oily injection suspensions may be administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension include, for example, sodium carboxymethyl cellulose, sorbitol, and/or dextran. Optionally, the suspension may also contain stabilizers.

[0200] Alternatively, NTP antisense RNA molecules, NTP ribozymes, and NTP EGS can be coded by DNA constructs which are administered in the form of virions, which are preferably incapable of replicating *in vivo* (see, for example, Taylor, WO 92/06693). For example, such DNA constructs may be administered using herpes-based viruses (Gage *et al.*, U.S. Patent No. 5,082,670). Alternatively, NTP antisense RNA sequences, NTP ribozymes, and NTP EGS can be coded by RNA constructs which are administered in the form of virions, such as retroviruses. The preparation of retroviral vectors is well known in the art (see, for example, Brown *et al.*, "Retroviral Vectors," in *DNA Cloning: A Practical Approach*, Volume 3, IRL Press, Washington, D.C. (1987)).

[0201] Specificity for gene expression in the central nervous system can be conferred by using appropriate cell-specific regulatory sequences, such as cell-specific enhancers and promoters. For example, such sequences include the sequences that regulate the oligodendroglial-specific expression of JC virus, glial-specific expression of the proteolipid protein, and the glial fibrillary acidic protein genes (Gage *et al.*, *supra*). Since protein phosphorylation is critical for neuronal regulation (Kennedy, "Second Messengers and Neuronal Function," in *An Introduction to Molecular Neurobiology*, Hall, Ed., Sinauer Associates, Inc. (1992)), protein kinase promoter sequences can be used to achieve sufficient levels of NTP gene expression.

[0202] Thus, gene therapy can be used to alleviate AD by inhibiting the inappropriate expression of a particular form of NTP. Moreover, gene therapy can be used to alleviate AD by providing the appropriate expression level of a particular form of NTP. In this case, particular NTP nucleic acid sequences may be coded by DNA or RNA constructs which are administered in the form of viruses, as described above. Alternatively, "donor cells" may be modified *in vitro* using viral or retroviral vectors containing NTP sequences, or using other well known techniques of introducing foreign DNA into cells (see, for example, Sambrook *et al.*, *supra*). Such donor cells include fibroblast cells, neuronal cells, glial cells, and connective tissue cells (Gage *et al.*, *supra*). Following genetic manipulation, the donor cells are grafted into the central nervous system and thus, the genetically-modified cells provide the therapeutic form of NTP (*Id.*).

[0203] Moreover, such virions may be introduced into the blood stream for delivery to the brain. This is accomplished through the osmotic disruption of the blood brain barrier prior to administration of the virions (see, for example, Neuwelt, United States Patent No. 4,866,042). The blood brain barrier may be disrupted by administration of a pharmaceutically effective, nontoxic hypertonic solution, such as mannitol, arabinose, or glycerol (*Id.*).

[0204] The following clones in *E. coli* were deposited according to the Budapest Treaty with the American Type Culture Collection (12301 Parklawn Drive, Rockville, Maryland, 20852): G2-2 PstI-DH5 (ATCC No. 69257); G5d-PstI-DH5 (ATCC No. 69258); 1-9a-LX-1 blue (ATCC No. 69259); AD3-4-DH1 (ATCC No. 69260); HB4-XL-blue (ATCC No. 69261); AD10-7-DH1 (ATCC No. 69262); AD2-2-DH 1- (ATCC No. 69263); GSd-1PstI-EcoRI-DHS (ATCC No. 69264); and G2-2PstI-EcoRI-DH5 (ATCC No. 69265).

[0205] Having now generally described the invention, the same will be more readily understood through reference to the following Examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Example 1

Expression of NTP Immunoreactivity, in Cell Lines

[0206] Seven cell lines of central nervous system origin were identified that express thread protein immunoreactivity using the Th9 monoclonal antibody which was generated to the pancreatic form of the protein (Gross *et al.*, *J. Clin. Invest.* 76:2115-2126 (1985)), but cross-reacts with thread proteins present in brain tissue and cerebrospinal fluid (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)). Among them were the following: two primitive neuroectodermal tumor (PNET) cell lines designated PNET1 and PNET2; three glioblastoma cell lines Hgl 16, Hgl 17, and C6; the A172 glial cell line; and the SH-Sy5y neuroblastoma cell line. The glioblastoma cell lines and the A172 cells were obtained from the American Type Culture Collection (ATCC). SH-Sy5y cells were obtained from Dr. Biedler at Sloan-Kettering Memorial Hospital. The PNET cell lines have been described previously (The *et al.*, *Nature genetics* 3:62-66 (1993)), and were obtained from Dr. Rene' Bernards at the MGH Cancer Center. All cell lines were maintained in Earl's Modified Eagle Medium supplemented with 10% fetal calf serum, and without antibiotics.

[0207] To examine the cells for thread protein and other immunoreactivities, the cultures were harvested in phosphate buffered saline (PBS) (137 mM NaCl, 2.7 mM KCl, 4.3 mM Na₂HPO₄, 1.4 mM KH₂PO₄, pH 7.3) containing 2 mM EDTA, and cytospin preparations were made using 10⁵ cells per slide. The cytospin preparations were fixed immediately in 100% methanol (-20°C), air-dried, and then stored at -80°C until used. Prior to immunostaining, the slides were equilibrated to room temperature and hydrated in PBS. Nonspecific antibody binding was blocked with 3 % nonimmune horse serum. Replicate cytospin preparations from the same cultures were incubated overnight at 4°C with 5 or 10 µg/ml of primary antibody. Immunoreactivity was revealed by the avidin-biotin horseradish peroxidase method using the Vectastain Elite kit (Vector Laboratories, Burlingame, CA) according to the manufacturer's protocol, and with 3-3' diaminobenzidine (0.5 mg/ml plus 0.03% hydrogen peroxide) as the chromogen. The cells then were counterstained with hematoxylin, dehydrated in graded alcohol solutions, cleared in xylenes, and preserved under coverglass with Permout (Fisher Scientific).

[0208] Cytospin preparations of each cell line were immunostained with the thread protein monoclonal antibodies Th9, Th7, Th10, Th29, Th34, TH46, Th67, and Th90. In addition, replicate slides were immunostained with positive (neurofilament, glial fibrillary acidic protein (GFAP), and vimentin) and negative (desmin, Hepatitis B surface antigen-5C3) control monoclonal antibodies. Except for 5C3 which was generated in the inventor's laboratory (Fujita *et al.*, *Gastroenterology* 91:1357-1363 (1986)), the control antibodies were purchased (Boehringer-Mannheim). All serological reagents were diluted in PBS containing 1 % bovine serum albumin (BSA), and all incubations except the one with primary antibody were carried out at room temperature in humidified chambers. The slides were washed in 3 changes of PBS between each step.

[0209] Both PNET1 and PNET2 cells expressed high and middle molecular weight neurofilament proteins and little or no glial fibrillary acidic protein or vimentin. The PNET1, PNET2, and SH-Sy5y cells expressed GAP-43, an abundant calmodulin-binding phosphoprotein that is highly expressed in immature neurons and in neurons undergoing regenerative cell growth (Benowitz *et al.*, *J. Neurosci.* 3:2153-2163 (1983); DeGraan *et al.*, *Neurosci. Lett.* 61:235-241 (1985); Kalil *et al.*, *J. Neurosci.* 6:2563-2570 (1986)). The A172 and C6 cells expressed GFAP and vimentin. However, A 172 also exhibited neurofilament immunoreactivity, raising doubt about its purely glial cell nature. None of the cell lines manifested immunoreactivity with monoclonal antibodies to desmin or to Hepatitis B surface antigen. As a negative control cell line, the Huh7 hepatocellular carcinoma cell line was similarly immunostained, and found not to exhibit any immunoreactivity with the above antibodies. However, the Huh cells were immunoreactive with monoclonal antibodies to the insulin receptor substrate protein, IRS-1 (data not shown) which was used as a positive control for this cell line

(Sasaki *et al.*, *J. Biol. Chem.* 268:1-4 (1993)). ' Using the Th9 monoclonal antibody, thread protein immunoreactivity was detected in primary PNET (A), primary glioblastoma (F), PNET1 (B), and C6 cells (G), but not in hepatocellular carcinoma cell lines (Figures 1A-1J). In addition, Th9 immunoreactivity was detected in histological sections from 8 of the 9 primary human CNS PNETs, and from all 5 of the primary human glioblastomas studied (Figures 1A-1J). Although all 5 cell lines exhibited intense immunoreactivity with the Th9 monoclonal antibody, they differed with respect to immunoreactivity for other Th monoclonal antibodies. The immunostaining reaction generated with the Th10 (C,H), Th7 (D,I), or Th46 monoclonal antibodies was either low-level (C,D) or absent (H,I,E,J) in PNET1 (C-E) and C6 (H-J). PNET2 cells exhibited only low levels of immunoreactivity with Th7 and Th29, and they manifested no immunostaining with the other Th monoclonal antibodies. A172, C6, and SH-Sy5y cells displayed little or no immunoreactivity with Th monoclonal antibodies other than Th9. Huh7 cells exhibited no immunoreactivity with any of the thread protein monoclonal antibodies employed, whereas human pancreatic tissue was immunoreactive with all of the Th antibodies, which had been generated against the purified pancreatic form of thread protein (Gross *et al.*, *J. Clin. Invest.* 76: 2115-2126 (1985)).

Example 2

Analysis of Thread Proteins by Monoclonal Antibody-Based Immunoradiometric Assay (M-IRMA)

[0210] Cultured cells were washed in PBS and recovered in PBS containing 2 mM EDTA. The cells were pelleted by centrifugation at 1000 x g for 15 min, and then resuspended in lysis buffer containing 50 mM Tris-HCl (pH 7.5), 1% Triton X-100, 2 mM EGTA, 10 mM EDTA, 100 mM NaF, 1 mM Na₄P₂O₇, 2 mM Na₃VO₄, 100 µg/ml phenylmethylsulfonyl fluoride, 1 µg/ml aprotinin, 1 µg/ml pepstatin A, and 1 µg/ml leupeptin. The supernatant fractions obtained by centrifugation of the lysates at 14,000 x g for 10 min were used for the Western blot analysis, immunoprecipitation studies, and M-IRMA. Protein concentration was determined by the Lowry colorimetric assay. The samples were stored at -40°C.

[0211] M-IRMA is a highly sensitive two- or three-site forward sandwich assay which permits quantitation of picomolar NTP in cell lysates, tissue culture medium, tissue homogenates, and body fluids (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992); Gross *et al.*, *J. Clin. Invest.* 76:2115-2126 (1985)). In addition, when combined with SDS-PAGE, M-IRMA can be used to determine molecular size of thread proteins and related species (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)). M-IRMA involves capturing the immunoreactive thread proteins present in biological samples using monoclonal antibodies Th7 and Th10 affixed to a solid-phase matrix, and then detecting the captured antigen with a third radiolabeled tracer monoclonal antibody (Th9) to the same protein. Briefly, 1/4" polystyrene beads (Precision Ball, Inc) were coated with one or two monoclonal antibodies to thread proteins (usually Th7 + Th10). Cell lysates or supernatant fractions of tissue homogenates (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)) were incubated over night with the coated beads to capture thread proteins present in the samples. The beads were washed 5x in PBS, and then incubated with ¹²⁵I labeled Th9 as a tracer to detect the captured thread proteins. The concentration of thread protein in the lysate or tissue homogenate was determined from a standard curve generated with known quantities of purified thread protein. This highly sensitive assay can detect as little as 10 pmol of thread protein in solution. To assay for thread proteins fractionated by SDS-PAGE, the wet gels were sliced at 2 mm intervals, and the proteins were eluted from each fraction into 0.5 ml of PBS by shaking for 24 hours at room temperature. The eluates were assayed directly for thread proteins by M-IRMA.

[0212] Corresponding with the widespread immunocytochemical staining of PNET1 cells with Th7, Th10, Th34, and Th29, thread protein immunoreactivity was readily measured in these cells by M-IRMA. In other words, with Th7, Th10, Th34, and Th29 monoclonal antibodies (MoAb) used as capture antibodies, either singularly or with two of them together, and ¹²⁵I labeled Th9 was used as the tracer, similarly high levels of thread protein were measured (Figure 2). In contrast, in PNET2, C6, and A172 cells, which exhibited intense immunoreactivity with Th9, but little or no immunocytochemical staining with the Th monoclonal antibodies that were used to capture antigen, the levels of thread protein detected by M-IRMA were much lower than those measured in the PNET1 cells (Figure 2). Similarly, Huh7 cells, which manifested no immunocytochemical staining with any of the thread protein monoclonal antibodies, had virtually non-detectable levels of thread proteins in the cellular lysates by M-IRMA. The concentrations of thread protein in the cell lysates were computed from a standard curve generated with purified PTP using Th7 and Th10 as capture antibodies. The results expressed as mean S.D. pg/mg of total protein were as follows: PNET1-13.1 ± 0.39; PNET2-2.06 ± 0.10; A172-3.38 ± 0.37; C6-2.52 ± 0.22; and Huh7-0.34 ± 0.05.

Example 3**Characterization of Neural Thread Proteins in Tumor Cell Lines**

[0213] In Western Blot analysis, samples containing 100 µg of protein were fractionated by SDS-PAGE, along with pre-labeled molecular weight standards. The proteins were blotted onto nylon membranes (Immobilon-P transfer membrane, Millipore) using a semi-dry transfer apparatus (Integrated Systems). The membranes were washed in Tris buffered saline (TBS; 10 mM Tris, 0.85% sodium chloride, pH 7.5), and then blocked with TBS containing 3% BSA. The blots were incubated overnight at 4°C with ¹²⁵I labeled Th9 monoclonal antibody. Unspecifically bound probe was removed by washing the membranes at room temperature in TBS-BSA 3 x 15 min, and 1 x 30 min. The results were analyzed by autoradiography using Kodak XAR film.

[0214] To prepare samples for immunoprecipitation studies, one milliliter samples of cell lysate containing approximately 1 mg/ml of protein were used for immunoprecipitation studies. The lysates were initially pre-cleared with non-relevant antibody (5C3 or antidesmin), and then with Protein A sepharose. Thread proteins were immunoprecipitated using 5-10 µg of Th9 and Protein A sepharose (Sasaki *et al.*, *J. Biol. Chem.* 268:1-4 (1993)). The immune complexes collected by centrifugation were resuspended in buffer containing 2% SDS and 10 mM β-mercaptoethanol, and then subjected to SDS-PAGE under denaturing and reducing conditions (*Id.*). Crude cellular lysates (100 µg protein) were analyzed simultaneously. The proteins were blotted onto Immobilon-P membranes and probed with ¹²⁵I labeled (*Id.*) Th9 to detect thread proteins and related molecules. Negative control experiments were performed simultaneously using either monoclonal antibodies to Hepatitis B surface antigen (5C3) or to desmin.

[0215] Metabolic labeling experiments were performed using monolayers of cells cultured in 100 mm² petri dishes. Prior to labeling, the cells were exposed to methionine- and cysteine-free medium for 2 h. The medium was then replaced with 3 ml of DMEM containing 300 µCi each of [³⁵S] methionine or [³⁵S] cysteine. After labeling for 3 hours, the cells were incubated for various intervals with complete medium devoid radiolabeled amino acids and supplemented with 10 mM methionine. Cell lysates were prepared as described above. Thread proteins were immunoprecipitated using the Th9 monoclonal antibody and protein A sepharose, and the immunoprecipitation products were analyzed by SDS-PAGE and film autoradiography.

[0216] For the *in vivo* phosphorylation studies, cells cultured as described for metabolic labeling studies were washed twice with TBS and incubated for 2 h with phosphate-free Dulbecco's MEM containing 10% dialyzed fetal calf serum. Then the cells were washed with TBS and incubated for 3 h with the same medium containing 400 µCi/ml of [³²P] orthophosphoric acid. The cell lysates were analyzed by immunoprecipitation with thread protein, and both positive (p36) and negative (desmin) control monoclonal antibodies, followed by SDS-PAGE.

[0217] In order to study the glycosylation state of neural thread proteins, cell culture lysates containing approximately 100 µg or protein were subjected to SDS-PAGE, and the fractionated proteins were transferred to Immobilon-P membranes (Millipore). O- and N-glycans were detected by periodate oxidation followed by biotinylation, and then Western blot analysis with a Streptavidin-alkaline phosphatase probe and NBT/BCIP as the colorimetric substrate. The assays were performed using the GlycoTrack Kit (Oxford Glycosystems, Rosedale, NY) according to the protocol provided by the manufacturer.

[0218] Th9-immunoreactive proteins were detected in lysates of PNET1, PNET2, SH-Sy5y, C6, and A172 cells by four different methods: Western blot analysis, immunoprecipitation followed by Western blot analysis, metabolic labeling followed by immunoprecipitation, and SDS-PAGE combined with M-IRMA. Western blot analysis of crude cellular lysates using ¹²⁵I-labeled Th9 demonstrated ~21 kDa bands in the above cell lines (as indicated by the arrow in Figure 3), but the signal intensity was low. In contrast, in lysates of human pancreatic tissue, the expected 17 kDa uncleaved and 14 kDa cleaved forms of pancreatic thread protein were readily detected by Western blot analysis (Figure 3). Thread proteins were not detected in lysates of human hepatocellular carcinoma cell lines. The strikingly greater abundance of thread proteins in pancreatic tissue compared with neuronal and glial cell lines is consistent with a previous finding of 10⁶-fold higher levels of thread proteins in pancreas and pancreatic juice compared with brain tissue and cerebrospinal fluid (Ozturk *et al.*, *Proc. Natl. Acad. Sci. USA* 86:419-423 (1989); de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990); de la Monte *et al.*, *J. Neurol. Sci.* 113:152-164 (1992); de la Monte *et al.*, *Ann. Neurol.* 32:733-742 (1992)). Although one would expect that thread proteins synthesized by PNET and glial cells are secreted as is the case for PTP and NTP, thread proteins were not detected in the tissue culture medium by Western blot analysis, even after concentrating the medium four- or five-fold by lyophilization.

[0219] Th9-immunoreactive thread proteins were more readily detected in PNET and glial cell lines by first immunoprecipitating from the lysates with either Th7+Th10 or Th9, and then performing Western blot analysis using ¹²⁵I-labeled Th9 (direct) (Figure 3), or unlabeled Th9 with ¹²⁵I-labeled Protein A (indirect). Both methods demonstrated 21 kDa thread protein-related species, similar to those detected by Western blot analysis. In addition, ~ 17 kDa bands were also observed in both PNET and glial cells, but the signal was inconsistent and low-level, as determined by Western blot analysis. As negative controls, the Huh7, HepG2, and FOCUS (Lun *et al.*, *In Vitro (Rockville)* 20:493-504 (1984))

human hepatocellular carcinoma cell lines were studied simultaneously under identical conditions, and Th9-immunoreactive proteins were not detected in the cellular lysates.

[0220] The molecular sizes of thread proteins present in PNET and glial cells were most prominently demonstrated by metabolic labeling with ^{35}S -methionine or ^{35}S -cysteine, followed by immunoprecipitation using Th9 monoclonal antibody. Monoclonal antibodies to desmin or to hepatitis B surface antigen (5C3) were used as negative controls for immunoprecipitation. In both PNET and glial cell lines, ~26 and ~21 kDa Th9-immunoreactive proteins were detected by SDS-PAGE analysis of the immunoprecipitated products (Figure 4B). In PNET1 cells, the 21 kDa band appeared as a doublet (Figure 4A); the accompanying slightly higher molecular weight species appeared to be less abundant than the dominant band at ~21 kDa. In addition, in both PNET and glial cell lines, there were also ~17 kDa Th9-immunoreactive proteins associated with bands of nearly the same intensity as the ~21 kDa bands. In C6 cells, there were also ~26 kDa, ~14-15 kDa and ~8 kDa Th9-immunoreactive proteins which were not detected in PNET cells (Figures 4A and 4B, arrows).

[0221] The 21 kDa and 17 kDa thread proteins in SH-Sy5y, PNET1, A172, and C6 cells, and their absence in hepatocellular carcinoma cells were also demonstrated by SDS-PAGE/M-IRMA (Figures 5A-5E). Cellular proteins fractionated by SDS-PAGE were eluted from the gels sliced at 2 mm intervals, and assayed directly for thread protein immunoreactivity by M-IRMA using Th7+Th10 as capture antibodies, and ^{125}I -labeled Th9 as the tracer. Despite low levels, two distinct peaks were evident in all neuroectodermal cell lines, but not in Huh7 hepatocellular carcinoma cells assayed simultaneously and in the same manner. The resolution of these gels did not permit distinction of ~17 kDa from ~14-15 kDa proteins which might have been present.

[0222] PNET1 and C6 cells were metabolically labeled with ^{32}P or ^{35}S -methionine, and thread proteins were immunoprecipitated from the lysates using Th9 monoclonal antibody (Figure 6). As a negative control, immunoprecipitation studies were conducted using an equal portion of the cellular lysate and monoclonal antibodies to desmin protein (Figure 6, right panel). In the cells labeled with ^{35}S methionine, Th9-immunoreactive bands were detected at ~26 kDa and ~21 kDa (upper arrows), ~17 kDa (lower arrows), and also at ~14-15 kDa (Figure 6). After ^{32}P labeling, only the 21 kDa band was observed by immunoprecipitation with Th9 monoclonal antibody; the other molecular weight species did not appear to be phosphorylated (Figure 6). Phosphorylated Th9-immunoreactive proteins were detected in C6 cells, but not in PNET1 cells, but this might be due to less efficient labeling since PNET1 cells grow slower than C6 cells. No bands in the 14 kDa to 26 kDa range were detected using monoclonal antibodies to desmin for immunoprecipitation (Figure 6). Carbohydrate moieties were not detected in Th9 immunoprecipitated proteins (data not shown).

[0223] The highest concentrations of thread protein were measured in subconfluent cultures of PNET1 cells, i.e. during the log phase of growth, and the lowest concentrations in overnight serum-starved cultures (growth arrest) (Figure 7). Cultures that were 100% confluent also had lower levels of thread protein expression compared with proliferating cultures. Huh7 hepatocellular carcinoma cells (negative control) were simultaneously studied using identical culture conditions, but the levels of thread protein remained low throughout.

[0224] Surprisingly, there was no change in the degree of thread protein immunocytochemical staining of PNET cells cultured under these various conditions. However, the degree to which the levels of thread proteins changed by M-IRMA measurement may not have been detectable by immunocytochemistry. Nevertheless, the reduction in cellular thread protein content induced by serum starvation was associated with a change in the phenotype of the cells. When the cells achieved 100 % confluence or after they had been subjected to overnight serum starvation, the cell bodies reduced in size, and they exhibited striking changes in the degree and distribution of immunoreactivity for neurofilament protein, GAP-43, and GFAP (Figure 8). In PNET cultures that were 50% confluent, the cells exhibited punctate and often a polar distribution of neurofilament and GAP-43 immunoreactivity, whereas 100% confluent and serum-starved PNET cultures exhibited diffuse perikaryal immunoreactivity for both neurofilament and GAP-43. The punctate immunoreactivity may have corresponded with distribution of neurofilament and GAP-43 in neurites. In contrast, 50% confluent PNET cultures were devoid of GFAP immunoreactivity, while 100% confluent and serum-starved cultures contained conspicuous proportions of GFAP-positive cells. Moreover, the proportion of GFAP-immunoreactive cells was greatest in 100% confluent serum-starved cultures, followed by 50% confluent serum-starved cultures, and then 100% confluent cultures with medium containing 10% fetal calf serum. Therefore, the reduction in thread protein levels measured in PNET cells subjected to overnight serum starvation may have been due to differentiation of the cells toward an astrocytic phenotype. C6 cells and other glioblastoma cell lines exhibited intense immunoreactivity with the Th9 monoclonal antibody, but the levels of thread protein measured by M-IRMA were often low, possibly due to low-level immunoreactivity with other thread protein antibodies, including Th7 and TH10 (see Figures 1A-1J).

Example 4

Cloning of Thread Proteins from Human cDNA Libraries

[0225] Human brain cDNA libraries made from 17-18 week old fetal brain (Stratagene, Inc., La Jolla, CA), 2 year-

old temporal lobe neocortex (Stratagene), and end-stage Alzheimer's disease cerebral cortex (In Vitrogen; San Diego, CA) were screened using probes generated from a 416 bp DNA fragment corresponding to nucleotides 235-650 of the rat PTP cDNA. The rat PTP cDNA, designated 018, was isolated from a rat pancreatic cDNA library using synthetic 60mer DNA probes corresponding to nucleotides 45-104 and 345-404 of the published sequence (Terazono *et al.*, *J. Biol. Chem.* 263:2111-2114 (1988); Watanabe *et al.*, *J. Biol. Chem.* 265:7432-7439 (1990)). Approximately 2×10^6 plaques or colonies from each library were screened with low-stringency hybridization using standard techniques (see Sambrook *et al.*, *supra*). Putative clones were plaque/colony purified, and the DNA inserts were sequenced by the dideoxynucleotide chain termination method using T7 polymerase (USB Sequenase; United States Biochemical Corp., Cleveland, OH). The sequences were compared with the Genebank database, and aligned with the nucleic acid sequences of other thread protein cDNAs.

1. CNS Neural Thread Protein cDNA Isolated from Human Fetal Brain Library

[0226] A 1.35 kilobase (kb) 1-9a CNS thread protein partial cDNA was isolated in which only a small segment corresponds to an open reading frame, and the remainder, to a 3' untranslated region (Figure 9A). The sequence of an additional 150 nucleotides was obtained from 5' anchor PCR amplification products. A second round of 5' anchor PCR amplification yielded a further upstream 600 bp product (Figure 9b). A portion of the 1-9a cDNA sequence shares significant homology with the 5' end of the human PTP cDNA and the Reg gene (Figure 10A). In addition, the initial 5' anchor PCR product has 60% homology with the 5' end of the Reg gene, and 63% homology with Exon 2 of the human Reg gene (Figure 10B). Moreover, probes generated from the 590 bp 5'-end fragment of 1-9a cDNA hybridized with human brain and pancreas mRNA (Figures 12A-12C). The 1-9a sequence is also homologous with the AD2-2 and AD3-4 cDNAs in that at one end of their completed sequences, the overlaps are substantial (Figure 10B).

2. CNS Neural Thread Protein cDNA Isolated from a Two-Year Old

Temporal Cortex Library

[0227] The HB4 clone is a 593 base pair partial cDNA that was isolated from a 2-year old temporal cortex library. This cDNA contains an open reading frame at its 5' end and terminates at nucleotide 275. There is a polyadenylation signal beginning at nucleotide 475, and the sequence ends with a poly-A tail (Figure 11D). The deduced amino acid sequence of the partial HB4 clone predicts a protein with a molecular weight of 10.4 kDa, and a pI of 12.1. The HB4 cDNA exhibits 50% overall nucleic acid homology with the human PTP cDNA (Figure 11E), a segment of the human Reg gene (Figure 11E).

3. Isolation of Neural Thread Protein cDNAs from an Alzheimer's Disease Library

[0228] Using the 018 rat PTP cDNA probe, four related cDNAs were isolated from an AD brain library. These clones were designated: AD 2-2, AD 3-4, AD 4-4 and AD 16c (also called AD 10-7) (Figures 16D-16S).

[0229] The AD 2-2 cDNA is approximately 1.2 kb and it shares significant homology with the 1-9a cDNA, AD 16c, rat PTP cDNA, and Exon 1 of the human Reg gene (Figure 17). The AD 2-2 probe generates a genomic Southern blot pattern similar to that obtained with the AD 3-4 probe. Figure 16E depicts the complete nucleotide sequence of the AD2-2 cDNA clone that was isolated from an AD brain library. Random primer generated probes based on this sequence hybridized with human brain and neuronal samples but not with glial cell lines or with pancreatic RNA.

[0230] Figures 16F, 16I, 16J and 16K depict partial nucleotide sequences of the AD3-4 cDNA clones that were isolated from an AD brain library. Random primer generated AD3-4 probes yielded two mRNA transcripts, 1.6 kb and 3.4 kb. These mRNA species are over-expressed in AD brains, with an average of two-fold elevation compared with aged matched control (N=8).

[0231] The AD 3-4 cDNA 1.6 kb clone is identical to another clone isolated at the same time (AD 5-3) (Figure 18A). The AD 3-4/AD 5-3 cDNA exhibits substantial homology with the 1-9a 5' anchor PCR products (Figure 18B), as well as with the human Reg gene and the Gen2a-EP genomic clone (Figure 18B). Southern blot analysis of human genomic DNA with the AD 3-4 probe revealed a pattern similar to that obtained with the AD 2-2 probe.

[0232] Figures 16L and 16M depict the partial nucleotide sequence of AD 4-4 which is a 0.8 kb partial cDNA clone which is identical to another cDNA isolated at the same time (AD 3-5). This AD 4-4 clone shares substantial sequence homology with AD 2-2 and 1-9a cDNAs (Figure 19). Figure 16N depicts the complete nucleotide sequence of a partial cDNA clone isolated from an AD brain library. This cDNA hybridized with brain and neuronal cell line mRNA, yielding a single 1.4 kb transcript.

[0233] Figure 16O depicts the nucleotide sequence of the 0.5 kb partial cDNA clone AD 16c (also called AD 10-7) that is 72% homologous with AD 2-2, and also aligns with human PTP and the human Reg gene sequences (Figures

20A and 20B).

[0234] Figure 16R depicts the complete nucleotide sequence of the AD10-7 clone that was isolated from an AD brain library. Hybridization of Northern blots using either antisense cRNA probes or random primer generated DNA probes detected 2.6, 1.9, 1.4 and 0.9 kb mRNA transcripts in neuronal cells. Neuronal cell lines expressed only the two largest transcripts, while mature adult human brains expressed predominantly the two smallest transcripts, and either very low or nondetectable levels of the 2.6 kb and 1.9 kb transcripts. Using an AD 10-7 probe, Northern blot analysis of RNA obtained from human liver, ovary, fallopian tube, colon, stomach, spleen, rectum, thyroid, 12 week placenta and kidney was negative.

[0235] Figure 16S depicts the complete nucleotide sequence of the AD16c cDNA clone that was isolated from an AD brain library. Hybridization of Northern blots using random primer generated DNA probes yielded the same results as obtained with the AD10-7 cDNA clone. The AD16c clone shares a 650 bp segment of near identity with AD10-7. In addition, elevated levels of AD16c mRNA were detected in AD brains compared with aged control brains by Northern blot analysis.

Example 5

Analysis of Brain Thread Protein Gene Expression

[0236] Thread protein mRNA expression was examined in the following neuroectodermal tumor derived cell lines: central nervous system primitive neuroectodermal tumor cells designated PNET1 and PNET2; HGL-16 and HGL-17 human glioblastoma cells; A172 human glioma cells; C6 rat glioma cells; and SH-Sy5y neuroblastoma cells. In addition, human brain tissue from patients with Alzheimer's disease or no neurological disease (aged controls), and embryonic and postnatally developing rat brain were assayed for thread protein mRNA expression. RNA extracted from human and rat pancreas served as positive controls.

[0237] RNA was extracted in 5 M guanidinium isothiocyanate, and then isolated by centrifugation through a cesium chloride step gradient (see Sambrook *et al.*, *supra*). RNA was quantified by measuring the absorbance at 260 nm and 280 nm. The thread protein mRNA transcript sizes were assessed by northern blot analysis, and the levels of expression were evaluated by RNA dot blot hybridization. Northern blot analysis was performed by electrophoresing samples containing 15 µg of total cellular RNA through 1% agarose-formaldehyde gels. The RNA was transferred to nylon membrane, cross-linked with ultraviolet light, and hybridized with probes generated from a 600 bp fragment of the 1-9A cDNA clone. The fragment used for hybridization studies contained the regions most homologous with the human PTP cDNA. The probes were labeled with [³²P] α-dCTP by the random primer method (Amersham Corporation; Arlington Heights, IL). The blots were hybridized overnight at 42°C with 2 x 10⁶ dpm /ml of probe in buffer containing 50% formamide, 5x SSPE, 10x Denhardt's (100x Denhardt's is 2% Ficoll, 2% bovine serum albumin, 2% polyvinylpyrrolidone), 0.5% SDS (sodium dodecyl sulfate), and 100 µg/ml of sheared denatured salmon sperm DNA. The membranes were washed in SSPE containing 0.25 % SDS using standard methods. Autoradiograms were generated by exposing the membranes to Kodak XAR film at -80°C. The membranes were subsequently stripped of probe and then rehybridized with a synthetic 30mer corresponding to 18s RNA to evaluate sample loading.

[0238] Northern analysis of total cellular RNA using probes made from the 1-9a cDNA disclosed two dominant transcripts in central nervous system (CNS) tumor cell lines: one transcript was 1.6 kb, and the other was 0.9 kb (Figure 12A). In addition, in the SH-Sy5y neuroblastoma and PNET1 cell lines, a larger 4.2 kb mRNA transcript was also detected. The 4.2 kb transcript may represent preprocessed mRNA. The same size transcripts were detected in adult (R. Brain) and newborn (NB) rat, but the 0.9 kb transcript was more abundant in the adult brain whereas the 1.6 kb transcript was more abundant in the newborn rat brain. In rat pancreas (R. Pane.), only a 0.9 kb transcript was detected, corresponding to the size of rat PTP mRNA (Terazono *et al.*, *J. Biol. Chem.* 263:2111-2114 (1988); Watanabe *et al.*, *J. Biol. Chem.* 265:7432-7439 (1990)). mRNA transcripts were not detected in normal liver (NI Liver). Using a probe generated from the 3' region of the 1-9a cDNA, the 1.6 kb, but not the 0.9 kb transcript was revealed (Figure 12B). Using a 30-mer probe corresponding to the most 5'-end of the 1-9a cDNA, the higher molecular weight mRNA transcripts were detected (Figure 12C). The 0.9 kb transcript was also evident with longer exposure of the blot.

[0239] Northern analysis of human brain RNA disclosed a dominant 1.6 kb transcript, but also two and sometimes three smaller transcripts of 1.2 kb, 0.9 kb, and 0.8 kb (Figure 13B). In contrast to the findings in cell lines, the 4.2 kb mRNA transcript was seldom observed in adult human brain. Hybridization with human pancreas disclosed a 0.8 kb transcript, corresponding with the size of PTP mRNA. The transcripts detected in human brain and pancreas using 1-9a probes were identical in size to the transcripts observed using PTP cDNA probes.

[0240] Dot blot RNA hybridization to 5 µg of total RNA using the 600 bp fragment of the 1-9a cDNA (NTP) demonstrated higher levels of expression in AD, compared with aged control brains (Figure 13A). Rehybridization of the same membrane with a cDNA corresponding to β-actin demonstrated similar loading of RNA in each dot. The observation of elevated levels of 1-9a-related mRNA in AD brain tissue is similar to that reported previously using 60mer probes

corresponding to human PTP cDNA (de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990)). The differences between AD and control brains appeared to be due to differences in the levels-of the 1.6 kb, 0.9 kb and 0.8 kb transcripts, as shown in Figures 13A and 13B.

[0241] The AD-NTP 3-4 cDNA, isolated from the AD library, hybridizes with RNA from neuronal-derived neuroectodermal tumor cell lines, and human brain tissue. In the cell lines, 1.6 kb and 0.9 kb transcripts as observed with the 1-9a probe were detected (Figure 21C). However, in human brain, ~4 kb, 1.6 kb, and 0.9 kb transcripts were detected, and the levels of expression for all three transcripts were higher in AD compared with aged control brains (Figure 21D).

[0242] AD 4-4 cDNA probe hybridized only with a 0.9 kb transcript, and only in neuronal cell lines.

Example 6

Direct Cloning and Sequencing of Thread Protein cDNAs from Neuroectodermal Tumor Cell Lines and Alzheimer's Disease Brain

[0243] Thread protein cDNAs were cloned directly from PNET1, PNET2, SH-Sy5y, and A172 cells, and from Alzheimer's disease and aged control brain RNA using the 3'- and 5'-RACE methods (Frohman *et al.*, *Proc. Natl. Acad. Sci. USA* 85:8998 (1988); Ohara *et al.*, *Proc. Natl. Acad. Sci. USA* 86:5673 (1989); Loh *et al.*, *Science* 243:217 (1989)). Briefly, RNA was reverse transcribed using oligo-dT primers. For the 5'-RACE reaction, the cDNAs were amplified by polymerase chain reaction (PCR) using a specific 17-mer corresponding to a 5'-region of the 1-9a sequence, and a 17 dT primer. The resulting PCR products were subjected to another round of amplification using another internal but overlapping 5'-end primer, and a specific 3'-17-mer corresponding to a 3' region of the 1-9a sequence. For the 3'-RACE reactions, the-cDNAs were first tailed with dCTP using terminal deoxynucleotide transferase, and then they were amplified using a specific 17-mer corresponding to nucleotides 781-797 of the 1-9a clone and dG (17mer). A second nested PCR amplification was performed using a specific 17mer corresponding to nucleotides 766-792 at the 3' end, and dGTP (17mer) for the 5' end. The PCR products were subjected to Southern blot analysis using probes generated from an internal DNA fragment of the 1-9a cDNA clone, and from the 018 rat PTP cDNA clone. The PCR products were gel purified and ligated into pAmpl vectors using uracil deoxytransferase. The subcloned DNA inserts were sequenced by the dideoxynucleotide chain termination method using T7 DNA polymerase.

[0244] CNS thread protein transcripts were detected in neuroectodermal tumor cell lines and in AD human brain tissue by reverse transcription followed by PCR using specific primers corresponding to the 5' and 3' regions of the 1-9a cDNA sequence. Southern blot analysis of the PCR products demonstrated two dominant cross-hybridizing species, 0.8 kb and 1.0 kb (Figures 14A and 14B). In addition, in the SH-Sy5y cells, a larger 1.8 kb PCR product was also detected. In the PNET1, PNET2, SH-Sy5y, and A172 cells, a 0.4 kb PCR product that hybridized with the 1-9a probe was observed. Corresponding with the higher levels of thread protein mRNAs in Alzheimer's disease brains, the hybridization signal was more intense in AD samples compared with aged control samples.

[0245] The PCR products generated from the SH-Sy5y cells were subcloned and sequenced. Southern analysis of the cloned fragments exhibited intense hybridization with the 1-9a cDNA, and less intense but definite hybridization with the 018 cDNA (rat PTP) (Figure 14C). The nucleic acid sequence of the SH-Sy5y PCR clone (Sy-NTP) was identical to the 1-9a cDNA sequence.

Example 7

Isolation of Genomic Clones Coding for Human Brain Thread Proteins

[0246] A human genomic DNA library was screened using probes made with a 600 bp fragment of the 1-9a human brain thread protein cDNA that was isolated from the two year-old temporal cortex library. The 1-9a cDNA fragment contained a region with 60% nucleic acid sequence homology with human PTP. After colony purification, the putative genomic clones were checked for cross-hybridization with the 018 rat PTP cDNA fragment. *EcoRI*, *PstI*, and *EcoRI/PstI* restriction fragments that hybridized with both the 1-9a and 018 probes were subcloned into pBluescript II vectors (Promega, Inc., Madison, WI) and then sequenced by the dideoxynucleotide chain termination method using either T7 polymerase (USE Sequenase) or polymerase chain reaction amplification and Vent polymerase.

[0247] Four genomic fragments designated G2-2 *PstI*, G2-2 *PstI-EcoRI*, G5d-1 *PstI*, and G5d-1 *PstI-EcoRI* were isolated from a human genomic DNA library (Figures 22A-22D). These genomic fragments all hybridized with both the 1-9a and 018 cDNA probes, and they ranged in size between 1.5 kb and 3 kb. Partial nucleic acid sequence information demonstrated homology between G2-2*PstI* and the human Reg gene and human and rat PTP cDNAs (Figure 23A); between G2-2 *PstI-EcoRI* and both the Reg gene and rat PTP cDNA (Figure 23B), and also with AD 2-2, AD 3-4, and the 1-9a cDNAs (data not shown); between G5d-1 *PstI* and the Reg gene and human PTP (Figure 23C); and between G5d-1 *PstI-EcoRI* and Reg gene, human PTP, 1-9a, and AD 4-4.

Example 8***In vitro Expression of the LacZ Fusion Protein and Demonstration of its Relatedness to Thread Proteins***

[0248] Fusion protein expression in bacteria containing the 1-9a cDNA clone, or one of the four genomic clones was induced with isopropylthio- β -D-galactoside (IPTG) using standard techniques (Sambrook *et al.*, *supra*). Crude bacterial lysates from induced and uninduced cultures were subjected to SDS-PAGE and Western blot analysis using the Th9 monoclonal antibody to thread protein (Sasaki *et al.*, *J. Biol. Chem.* 268:1-4 (1993)), and 125 -I labeled protein A to detect the bound antibody. In addition, bacterial lawns containing cloned DNA were induced to express the fusion protein with IPTG, and replica filters were probed directly with Th9 monoclonal antibody followed by 125 -I labeled protein A.

[0249] Thread protein immunoreactivity was demonstrated in the bacterial fusion proteins by direct antibody binding to the IPTG-induced colonies (Figures 24A-24D). Thread protein immunoreactivity was detected using a cocktail of Th9, Th7, and Th10 monoclonal antibodies to PTP (Sasaki *et al.*, *J. Biol. Chem.* 268:1-4 (1993), and 125 -I labeled Protein A.

Example 9***Relative Levels of AD16c mRNA in AD and Aged Control Brains***

[0250] Northern blot analysis was performed using an AD16 cDNA probe. The blots were re-probed to detect 18s ribosomal RNA to evaluate loading of RNA in each lane. The unsaturated autoradiograms were subjected to densitometric analysis using a Molecular Dynamics Image Analyzer. The ratios of the AD16c and 18s RNA hybridization signals were plotted for each case, and the results are depicted graphically in Figures 25A and 25B. The mean ratios (relative levels of AD16c) with standard errors are depicted in the smaller right hand graph. The findings confirm that there are elevated levels of AD16c mRNA expression in 6 of 9 AD brains compared to 1 of 6 age-matched controls. The difference between the mean levels is highly statistically significant ($P < 0.005$). Similar results were obtained using AD10-7 probes. These results demonstrate that there is a statistically significant increase in levels of expression in AD brains compared to control brains.

Example 10***Preparation of Recombinant AD10-7 Fusion Protein and Detection Thereof With Monoclonal Antibodies***

[0251] AD10-7 cDNA was ligated into pTrcHIS vectors (In Vitrogen, San Diego) in three different reading frames (two incorrect-A and B, and one correct-C). Bacteria transformed with one of three plasmids were induced with IPTG and bacterial lysates were examined for protein expression 0, 1 and 5 hours later. The proteins were fractionated by SDS-PAGE, and Western blot analysis was performed using monoclonal antibodies against the expressed tag protein (T7-tag mouse monoclonal antibodies; Novogen). The blots were developed using the avidin-biotin, horseradish peroxidase method, with diaminobenzidine as the chromogen (Figure 26). A band corresponding to ~45 kDa was detected in bacteria that had been transformed with plasmid DNA which contained AD10-7 ligated only in the correct reading frame (C) (arrow). The same size protein was observed by *in vitro* translation of the AD10-7 cDNA in a rabbit reticulocyte lysate assay system. In both systems, the fusion partner peptide was ~3 kDa, indicating that the cDNA encodes a protein of about ~42 kDa. A ~42 kDa NPT species is routinely detected by Western Blot analysis of neuronal cell lines and of human brain tissue.

Example 11***Demonstration of Neuronal Localization of AD10-7 mRNA Expression by In Situ Hybridization***

[0252] Sense and antisense cRNA probes were generated from linearized AD10-7 plasmid DNA using SP6 or T7 DNA-dependent RNA polymerase, respectively. The antisense probes hybridized with neuronal cell line mRNA as described above for this clone. The cRNA sense probes, on the other hand, failed to hybridize with RNA by Northern blot analysis. cRNA probes labeled with digoxigenin-UTP were hybridized with human brain tissue sections from early AD. After washing the sections extensively (de la Monte *et al.*, *J. Clin. Invest.* 86:1004-1013 (1990)), the hybridized probes were detected using peroxidase or alkaline phosphatase conjugated monoclonal antibodies to digoxigenin, and the colorimetric reactions were revealed using standard methods. Examination of the sections by brightfield and dark-field microscopy demonstrated hybridization of AD10-7 only in neurons (Fig. 27; dense aggregates of white grains over

cell bodies in (Fig. 27A)). In contrast, and similar to the findings by Northern blot analysis, the *sense* AD10-7 cRNA probes failed to hybridize with brain tissue (Fig. 27B).

[0253] Although the foregoing refers to particular preferred embodiments, it will be understood that the present invention is not so limited. It will occur to those of ordinary skill in the art that various modifications may be made to the disclosed embodiments and that such modifications are intended to be within the scope of the present invention, which is defined by the following Claims.

[0254] All publications and patent applications mentioned in this specification are indicative of the level of skill of those in the art to which the invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference in their entirety.

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

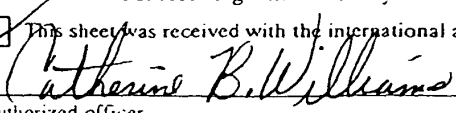
(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>9</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69257
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: G2-2PstI-DH5	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application <i>Catherine B. Williams</i> Authorized officer	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: _____ Authorized officer

Form PCT/RO/134 (July 1992)

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

5	A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>10</u>	
10	B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
	Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
15	Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
20	Date of deposit 16 March 1993	Accession Number 69258
25	C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
30	Escherichia coli: G5d-PstI-DH5	
35	D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
40	E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
45	The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
50	For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application  Authorized officer	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer
55		

Form PCT/RO/132 (July 1992)

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>10</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69259
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: 1-9a-LX-1 blue	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
<input checked="" type="checkbox"/> For receiving Office use only This sheet was received with the international application <i>Catherine B. Williams</i> Authorized officer	<input type="checkbox"/> For International Bureau use only This sheet was received by the International Bureau on: Authorized officer

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>10</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69260
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: AD3-4-DH1	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
For receiving Office use only	
For International Bureau use only	
<input checked="" type="checkbox"/> This sheet was received with the international application <i>Catherine R. Williams</i> Authorized officer	<input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

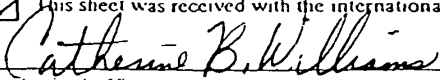
(PCT Rule 13bis)

5	A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>11</u>	
10	B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
	Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
15	Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
20	Date of deposit 16 March 1993	Accession Number 69261
25	C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
30	Escherichia coli: HB4-XL-blue	
35	D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
40	E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
45	The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
50	For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application <i>Catherine B. Williams</i> Authorized officer	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer:
55		

Form PCT/RO/134 (July 1992)

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

5	A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>11</u>	
10	B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
	Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
15	Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
20	Date of deposit 16 March 1993	Accession Number 69262
25	C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
30	Escherichia coli: AD10-7-DH1	
35	D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
40	E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
45	The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
50	For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application  Authorized officer	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer
55		

Form PCT/RO/134 (July 1992)

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>12</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit 16 March 1993	Accession Number 69263
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli: AD2-2-DH1	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
<input checked="" type="checkbox"/> For receiving Office use only This sheet was received with the international application <i>Catherine B. Williams</i> Authorized officer	<input type="checkbox"/> For International Bureau use only This sheet was received by the International Bureau on: _____ Authorized officer

Form PCT/RO/134 (July 1992)

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

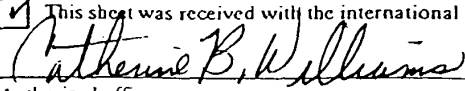
(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>12</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>AMERICAN TYPE CULTURE COLLECTION</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>16 March 1993</u>	Accession Number <u>69264</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<u>Escherichia coli: G5d-1PstI-EcoRI-DH5</u>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application <u>Catherine B. Williams</u> Authorized officer	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer
---	---

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

5	A. The indications made below relate to the microorganism referred to in the description on page <u>56</u> , line <u>13</u>	
10	B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
	Name of depositary institution AMERICAN TYPE CULTURE COLLECTION	
15	Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
20	Date of deposit 16 March 1993	Accession Number 69265
25	C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
30	Escherichia coli: G2-2PstI-EcoRI-DH5	
35	D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
40	E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
45	The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
50	For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application  Authorized officer	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer
55		

Annex to the application documents - subsequently filed sequences listing

[0255]

5

10

15

20

25

30

35

40

45

50

55

SEQUENCE LISTING

5 <110> The General Hospital Corporation
de la Monte, Suzanne
Wands, Jack R.

<120> Neural Thread Protein Gene Expression and Detection
of Alzheimer's Disease

10 <130> P19088EP-1/PWC

<140> EP 04076254.4
<141> 1994-04-20

15 <150> US 08/050,559
<151> 1993-04-20

<160> 121

20 <170> PatentIn version 3.2

<210> 1
<211> 21
<212> DNA
<213> Homo sapiens

25 <400> 1
ccgattccaa cagaccatca t 21

<210> 2
30 <211> 21
<212> DNA
<213> Homo sapiens

<400> 2
35 ccaacagacc atcattccac c 21

<210> 3
<211> 21
<212> DNA
40 <213> Homo sapiens

<400> 3
ccaaaccgat tccaacagac c 21

45 <210> 4
<211> 30
<212> DNA
<213> Homo sapiens

50 <400> 4
cctgggcaac aagagcgaaa actccatctc 30

<210> 5
55 <211> 30
<212> DNA

EP 1 564 293 A1

5 <213> Homo sapiens
 <400> 5
 atcgcttgaa cccgggaggc ggaggttgcg 30

 10 <210> 6
 <211> 30
 <212> DNA
 <213> Homo sapiens

 <400> 6
 ggggaggctg aggcaggaga atcgcttgaa 30

 15 <210> 7
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 20 <220>
 <223> Triple helix-forming oligonucleotide

 <220>
 <221> misc_feature
 25 <222> (1)..(21)
 <223> This region is in the 3' to 5' orientation

 <220>
 <221> misc_feature
 <222> (22)..(22)
 30 <223> May be a 0-10 base oligonucleotide linkage between
 oligonucleotides

 <400> 7
 tactaccaga caaccttagc cnccgattcc aacagaccat cat 43

 35 <210> 8
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 40 <220>
 <223> Triple helix-forming oligonucleotide

 <220>
 45 <221> misc_feature
 <222> (22)..(22)
 <223> May be a 0-10 base oligonucleotide linkage between
 oligonucleotides

 <220>
 50 <221> misc_feature
 <222> (23)..(43)
 <223> This region is in the 3' to 5' orientation

 <400> 8
 55 ccgattccaa cagaccatca tntactacca gacaacctta gcc 43

EP 1 564 293 A1

```

5    <210> 9
    <211> 43
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Triple helix-forming oligonucleotide

10   <220>
    <221> misc_feature
    <222> (1)..(21)
    <223> This region is in the 3' to 5' orientation

15   <220>
    <221> misc_feature
    <222> (22)..(22)
    <223> May be a 0-10 base oligonucleotide linkage between
        oligonucleotides

20   <400> 9
    ccaccttact accagacaac cnccaacaga ccatcattcc acc 43

    <210> 10
    <211> 43
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Triple helix-forming oligonucleotide

30   <220>
    <221> misc_feature
    <222> (22)..(22)
    <223> May be a 0-10 base oligonucleotide linkage between
        oligonucleotides

35   <220>
    <221> misc_feature
    <222> (23)..(43)
    <223> This region is in the 3' to 5' orientation

40   <400> 10
    ccaacagacc atcattccac cnccacctta ctaccagaca acc 43

45   <210> 11
    <211> 43
    <212> DNA
    <213> Artificial Sequence

50   <220>
    <223> Triple helix-forming oligonucleotide

    <220>
55   <221> misc_feature

```

EP 1 564 293 A1

<222> (1)..(21)
 <223> This region is in the 3' to 5' orientation

5 <220>
 <221> misc_feature
 <222> (22)..(22)
 <223> May be a 0-10 base oligonucleotide linkage between
 oligonucleotides

10 <400> 11
 ccagacaacc ttagccaaac cnccaaaccg attccaacag acc 43

15 <210> 12
 <211> 43
 <212> DNA
 <213> Artificial Sequence

20 <220>
 <223> Triple helix-forming oligonucleotide

25 <220>
 <221> misc_feature
 <222> (22)..(22)
 <223> May be a 0-10 base oligonucleotide linkage between
 oligonucleotides

30 <220>
 <221> misc_feature
 <222> (23)..(43)
 <223> This region is in the 3' to 5' orientation

<400> 12
 ccaaaccgat tccaacagac cnccagacaa ccttagccaa acc 43

35 <210> 13
 <211> 1443
 <212> DNA
 <213> Homo sapiens

40 <400> 13
 cgctgcgccc aggctggctc tggaaagcct gtgcggctct ggcaggaagc ccggcccgtg 60
 gagcagggttt tcgttctgct tcagcaataa ataagggtga ccacagggac tttgcttttg 120
 gtttcctttc ctgtgaaaag gttggtttta aagttagata cacttttccg tagaacaagt 180
 45 gttctatctt taaaaaccca aattgcagca ccgtggatta ctggtctcag aacaactcat 240
 tgcgcacatcag atttgactct ctgattttct gtctattggc caaattgcc tttaactgca 300
 cctgaatcct ttgtgtactg atgcctttga gctgggcacc ttgggagagt gttgtgttg 360
 50 tgtttacggt tcttccttcc ccttgctaata tacagtctct ggtgccccagc aagccccttt 420
 ggcttccttc cgtgactggt cacgttgtct gcctgggctc agcgtggacc tgcccatgc 480
 55 tgcagaacct ggcctcacct ggacttttac tagaattgcc agcttctcaa cttagcagat 540

EP 1 564 293 A1

```

catcactcat gcgggcacaa gcaaagatca acactttctt ttttggttaag cttgagtttt 600
acaagttatt ttttggtgat gcgtaagaca ttgcagtggg aaaccattca acttgagttt 660
5 attggagttt gctgtttag caggtttta ctcaggaaca actcttgtct gatctctcgc 720
ccctctgccg ggactacatt actgtctctc ggagccggtg gcgttgctgt cgagtcccag 780
gactatctct gcagactgct atgctcagat cgaagtattt cacaagaata cttgtgtttt 840
10 taacagccct tcccctggac ggtgcgccat gagggcctca tggtacgcat tgccttttct 900
ttctgtggat ccagtatctt cctcggcttt ttagggagca ggaaaaatgc gtctgagagc 960
aactcttttt aaaaacctgc cctgttgtat ataactgtgt ctgtttcacc gtgtgacctc 1020
15 caaggggggtg ggaacttgat ataaacgttt aaagggggcca cgatttgccc gagggttact 1080
cctttgctct caccttgtat ggatgaggag atgaagccat ttcttatcct gtagatgtga 1140
agcactttca gttttcagcg atgttgaat gtagcatcag aagctcgttc cttcacactc 1200
20 agtggcgctc gtgcttgctc acatgcgctg ggcgtctgga ccttgaatgc ctgccctggt 1260
tgtgtggact ccttaatgcc aatcatttct tcaacttctc ggacaccag ggcgcctgtt 1320
gacaagtgtg gagaaactcc taatttaa atgtcagaca atgtcctagt gttgactact 1380
25 acaatgttga tgctacactg ttgtaattat taaactgatt atttttctta tgtcaaaaaa 1440
aaa 1443
30
<210> 14
<211> 213
<212> DNA
<213> Homo sapiens
35
<400> 14
gatcccgttt gacaggtgta ccgccccagt caaactcccc acctggcact gtccccggag 60
cggtcgcgcc cgcgcgacca cggagctctg ggcgccagaa gcgagagccc ctgcgtgccc 120
40 cccgcctcac cgggtagtga aaaaacgatg agagtagtgg tatttcaccg gcggcccgcg 180
aggacccccg cccgaccag tgcggaacgg ggg 213
45
<210> 15
<211> 358
<212> DNA
<213> Homo sapiens
50
<220>
<221> misc_feature
<222> (56)..(56)
<223> n is a, c, g, or t
55
<400> 15
cacctggat tactggctc agaacaactc attgcgcac agatttactc tctgantttc 60

```

EP 1 564 293 A1

tgtctattgg ccattgccct ttaactgcac ctgaatcctt tgtgtactga tcctttgagc 120
 tggggcacctt gggagagtgt tgtgttgctg tttacgggtc ttccttcccc ttgctaatta 180
 5 cagtctctgg tgccagcaag cccctttggc ttccttccgt gactgggcac gttgtctgcc 240
 tggggccagcg tggcccatg ctgcagaacc tggcctcagg acttttcact agaattgccc 300
 10 ttcctcaact tagcagatca ttcactcatg cgggcacaag caaagatcaa cactttct 358

 <210> 16
 <211> 378
 <212> DNA
 15 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (242)..(242)
 20 <223> n is a, c, g, or t

 <400> 16
 cattgcagct cagcatggct cagaccagct catacttcat gctgatctcc tgcctgatgt 60
 25 ttctgtctca gagccaaggc caagaggccc agacagagtt gcccaggcc cggatcagct 120
 gcccagaagg caccaatgcc tatcgctcct actgctacta ctttaatgaa gaccgtgaga 180
 cctgggttga tgcagatctc tattgccaga acatgaattc gggcaacctg gtgtctgtgc 240
 30 tnccaggcc gagggcctt ttgtggcctc actgattaag gagagtggca ctgatgactt 300
 caatgtctgg attggcctcc atgaccccaa aaagaaccgc cgctggcact ggagcagtgg 360
 gtccttggtc tcctacaa 378
 35
 <210> 17
 <211> 142
 <212> DNA
 <213> Homo sapiens
 40
 <400> 17
 ttttcctaga acaagggttc tatctttaaa aacccaaatt gcagcaccgc tggcttcaga 60
 acaactcatt gcgcatcaga tttactctct gatttttctg tctatattggc caaattgccc 120
 45 ttttaactgc acctgaatct tt 142

 <210> 18
 <211> 151
 <212> DNA
 50 <213> Homo sapiens

 <400> 18
 ttctcctata gagattgttg atttgctct tagcaagaga ttcattgcag ctcagcatgg 60
 55 ctcagaccag ctcatcttc atgctgatct cctgcctgat gtttctgtct cagagccaag 120

EP 1 564 293 A1

gtaagatctc ttttccacca accaactctt t 151

5 <210> 19
<211> 75
<212> DNA
<213> Homo sapiens

10 <400> 19
caccgtggat tactgggtctc agaacaactc attgcgcacg agatttactc tctgattttt 60
ctgtctattg gccaa 75

15 <210> 20
<211> 77
<212> DNA
<213> Homo sapiens

20 <400> 20
cattgcagct cagcatggct cagaccagct catacttcat gctgatctcc tgcctgatgt 60
ttctgtctca gagcaa 77

25 <210> 21
<211> 130
<212> DNA
<213> Homo sapiens

30 <400> 21
gaattcctgg gctcaagtga tcctctcatg cagtctccca aagtgctggg atgacaggct 60
tgagccacca caccaggccc atcatcagtt tatataaaga aaaaaaaacc ttaaaattgt 120
taggcaaata 130

35 <210> 22
<211> 144
<212> DNA
<213> Homo sapiens

40 <400> 22
ggagttttgt catcaggcca gcctcatccc gaggtctcct ccaccattgg ccgtagccag 60
caggttcagt gtcaccgaa agtaaaatcc cctccttcag caagaataaa gcaatataca 120

45 ccttaggttc cactaagtaa cata 144

50 <210> 23
<211> 96
<212> DNA
<213> Homo sapiens

<400> 23
gttctgtgag tctcaatttg ttcttctctg gaagctgtct ggtgaatctg ttggtccttc 60

55 tgtctgctat tctgtctgtc tgtatgtctg tccatg 96

EP 1 564 293 A1

<210> 24
 <211> 105
 <212> DNA
 5 <213> Homo sapiens

 <400> 24
 gttgatttgc ctcttaagca agagattcat tgcagctcag catggctcag accagctcat 60
 10 acttcatgct gatctcctgc ctgatgtttc tgtctcagag ccaag 105

 <210> 25
 <211> 215
 <212> DNA
 15 <213> Homo sapiens

 <400> 25
 actaccaaac ctgcattaac aaatttcggt tggtcgacct cggagcagaa cccaacctcc 60
 20 gagcagtaca tgctaagact tcaccagtca aagcgaacgt actatactca attgatccaa 120
 taacttgacc aacggaacaa gttaccctat aacagcgcaa tcctattcta gagtccatat 180
 caacagggtt tacgacctcg atgttggatc aggac 215
 25
 <210> 26
 <211> 232
 <212> DNA
 <213> Homo sapiens
 30
 <400> 26
 accacggagc tctgggcgcc agaagcgaga gcccctcgct gcccccgcc tcaccgggta 60
 gtgaaaaaac gatgagagta gtggtatttc accggcgcc cgcgaggacc cccgccccgac 120
 35 ccagtgcgga acgggggaggt agtcccgggg gctcacttat tctacattag tctcacgtgc 180
 agactagagt caagctcaac agggctcttct ttcccgtga ttccgccaag tc 232
 40
 <210> 27
 <211> 112
 <212> DNA
 <213> Homo sapiens
 45
 <400> 27
 agtttcactc tggtgcccag gctggagtgc aatggcaca tcctggctca ctgcaacctc 60
 cgctcccga gctcaagcaa ttctcctgcc tcagcctcgt gagccgctgg ga 112
 50
 <210> 28
 <211> 120
 <212> DNA
 <213> Homo sapiens
 55
 <400> 28
 agatctcgct ctgtcaccga ggctgaagtg cagtggccca atctcggtc actgcgagct 60

EP 1 564 293 A1

ccacctcccg ggttcacttc attctcctgc ctcaactgcct cagcctctga gtagctggga 120

5 <210> 29
 <211> 594
 <212> DNA
 <213> Homo sapiens

10 <400> 29
 gaggcgtatt ataccatgct ccatctgcct acgacaaaca gacctaaaat cgctcattgc 60
 atactcttca atcagccaca tagccctcgt agtaacagcc attctcatcc aaacccccctg 120
 aagcttcacc ggcgcagtca ttctcataat cgcccacggg cttacatcct cattactatt 180
 15 ctgcctagca aactcaaact acgaacgcac tcacagtcgc atcataatcc tctctcaagg 240
 acttcaaact ctactcccac taatagcttt ttgatgactt ctagcaagcc tcgctaacct 300
 cgccttacct cccactatta acctactggg agaactctct gtgctagtaa ccacgttctc 360
 20 ctgatcaaat atcactctcc tacttacagg actcaacata ctagtcacag ccctatactc 420
 cctctacata ttaccacaa cacaatgggg ctcaactcacc caccacatta acaacataaa 480
 25 accctcattc acacgagaaa acaccctcat gttcatacac ctatccccca ttctcctcct 540
 atccctcaac cccgacatca ttaccggggtt ttctctctaa aaaaaaaaaa aaaa 594

30 <210> 30
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 30

35 Glu Ala Tyr Tyr Thr Met Leu His Leu Pro Thr Thr Asn Arg Pro Lys
 1 5 10 15

40 Ile Ala His Cys Ile Leu Phe Asn Gln Pro His Ser Pro Arg Ser Asn
 20 25 30

Ser His Ser His Pro Asn Pro Leu Lys Leu His Arg Arg Ser His Ser
 35 40 45

45 His Asn Arg Pro Arg Ala Tyr Ile Leu Ile Thr Ile Leu Pro Ser Lys
 50 55 60

50 Leu Lys Leu Arg Thr His Ser Gln Ser His His Asn Pro Leu Ser Arg
 65 70 75 80

55 Thr Ser Asn Ser Thr Pro Thr Asn Ser Phe Leu Met Thr Ser Ser Lys
 85 90 95

EP 1 564 293 A1

Pro Arg

5
 <210> 31
 <211> 554
 <212> DNA
 <213> Homo sapiens

10
 <220>
 <221> misc_feature
 <222> (176)..(176)
 <223> n is a, c, g, or t

15
 <400> 31
 ataccatgct ccattctgcct acgacaaaca gacctaaaat cgctcattgc atactcttca 60
 atcagcacat agccctcgta gtaacagcca ttctcatcca aacccctga agcttcaccg 120
 20 ggcagtcatt tctcataatc gcccacgggc ttacatcctc attactattc tgccancaaa 180
 ctcaaactac gaacgcactc acagtgcgat cataatctct ctcaaggact tcaaactcta 240
 ctcccaagct ttgtgacttc tagcaacctc gctaacctcg ccttaccctc actattaact 300
 25 actgggagaa tgtgctagta accacgttct ccttcaaata tcaactctct acttacagga 360
 ctcaacatac tagtccagcc ctatactccc tctacatatt taccacaaca caatgggctc 420
 actcaccacac cacattaacc ataaaaccct cattcacacg agaaaacacc ctcatgttca 480
 30 tacacctatc cccattctt cctatccctc aaccccgaca tcaaccgggt ttcctcttaa 540
 aaaaaaaaaa aaaa 554

35
 <210> 32
 <211> 590
 <212> DNA
 <213> Homo sapiens

40
 <400> 32
 atgcctatcg ctctactgc tactacttta atgaagaccg tgagacctgg gttgatgcag 60
 atctctattg ccagaacatg aattcgggca acctgggtgc tgtgctcacc caggccgagg 120
 gtgcctttgt ggcctcactg attaaggaga gtggcactga tgacttcaat gtctggattg 180
 45 gcctccatga ccccaaaaag aaccgccgct ggactggag cagtgggtcc ctgggtctct 240
 acaagtcttg gggcattgga gcccgaagca gtgttaatcc tggctactgt gtgagcctga 300
 cctcaagcac aggattccag aaatggaagg atgtgccttg tgaagacaag ttctcctttg 360
 50 tctgcaagtt caaaaactag aggcagctgg aaaatacatg tctagaactg atccagcaat 420
 tacaacggag tcaaaaatta aaccggacca tctctccaac tcaactcaac ctggacactc 480
 tcttctctgc tgagtttgcc ttgttaatct tcaatagttt tacctacccc agtctttgga 540
 55

EP 1 564 293 A1

accttaaata ataaaaataa acatgtttcc actaaaaaaa aaaaaaaaaa 590

5 <210> 33
 <211> 466
 <212> DNA
 <213> Homo sapiens

10 <400> 33
 cttctttttc aggccaagag gccagacag agttgcccc ggcccggatc agctgcccag 60
 aaggcaccaa cctatcgctc ctactgctac tactttaatg aagaccgca gacctggggtt 120
 gatgcagtgt gaggtaggag agcgtgtggg aaggagact catgaaggga gggaagctg 180
 15 ccactctcca gtgttcagt ggcgaatgag atgagactga acccctttat actatcatca 240
 gccccaaact ttccaatcta ctttatccca ttattcagca cattcccagc acaaagaacc 300
 tgggtgggtga cagcatcatc acggacatta ctctgctgtc ctttttcacc ctctcttgg 360
 20 aggactcagt atatccgtca caaccctcca ctgagtctcc attttcttct gcaacagctc 420
 tattgccaga acatgaattc gggcaacctg gtgtctgtgc tcaccc 466

25 <210> 34
 <211> 501
 <212> DNA
 <213> Homo sapiens

30 <220>
 <221> misc_feature
 <222> (123)..(123)
 <223> n is a, c, g, or t

35 <400> 34
 cgtattatac catgctccat ctgcctacga caaacagacc taaaatcgct cattgcatac 60
 tcttcaatca gccacatagc cctcgtagta acagccattc tcatccaaac cccctgaagc 120
 40 ttncgggcgc agtcattctc ataatcgccc acgggcttac atcctcatta ctattctgcc 180
 tagcaaactc aaactacgaa cgcactcaca gtcgcatcat aatcctctct caaggacttc 240
 aaactctact ccactaata gttttttgat gacttctagc aagcctcgct aacctcgctt 300
 45 tccccccac tattaaccta ctgggagaac tctctgtgct agtaaccagc ttctcctgat 360
 caaatatcac tctctactt acaggactca acatactagt cacagcccta tactccctct 420
 acatatttac cacaacacaa tggggctcac tcaccacca cattaacaac ataaaaccct 480
 50 cattcacag agaaaacacc c 501

55 <210> 35
 <211> 372
 <212> DNA

EP 1 564 293 A1

<213> Homo sapiens

<400> 35
5 gttcttagtc tatctcttgt acaaacgatg tgctttgaag atgttagtgt ataacaattg 60
atgtttgttt tctgtttgat tttaaacaga gaaaaaataa aagggggtaa tagctccttt 120
tttcttcttt cttttttttt ttcatttcaa aattgctgcc agtgttttca atgtaggaca 180
10 acagagggat atgctgtaga gtgtttttat tgcctagttg acaaagctgc ttttgaatgc 240
tggtggttct attcctttgc acatcacgac attttataat catagttaaa tcgtatatga 300
caaaaatgct ctgatctgat gccaaagggtc aattcagtgt atataacctg aacacactca 360
15 tccattgcgt tt 372

<210> 36
<211> 68
20 <212> PRT
<213> Homo sapiens

<400> 36

Met Phe Val Phe Cys Leu Ile Leu Asn Arg Glu Lys Ile Lys Gly Gly
25 1 5 10 15

Asn Ser Ser Phe Phe Leu Leu Ser Phe Phe Phe Ser Phe Gln Asn Cys
30 20 25 30

Cys Gln Cys Phe Gln Cys Arg Thr Thr Glu Gly Tyr Ala Val Glu Cys
35 35 40 45

Phe Tyr Cys Leu Val Asp Lys Ala Ala Phe Glu Cys Trp Trp Phe Tyr
40 50 55 60

Ser Phe Asp Thr
40 65

<210> 37
<211> 377
45 <212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (59)..(59)
50 <223> n is a, c, g, or t

<400> 37
actgtctccc cctttgatag ggacactaaa gtggctctgta cttgggtaga ggatggcang 60
55 ttaagaatta aaatcgtctg ggtgcggtct gcacgcttgt aatcccagca ctttgggagg 120

EP 1 564 293 A1

ctgaggcggg cggatcacct gaggtcagga gttcgacacc agcctgatga acatggagaa 180

accccatctc tactaaaaat acaaatatta gctgggcgtt gtcgcgcgcc tgtaatccca 240

5 gcggtctcacg aggctgaggc aggagaattg cttgagctcg ggatggcgga ggttgcaagtg 300

agccaggatt gtgccattgc actccagcct gggcaacaag agtgaaactc tgtctcaaaa 360

aaaaaaaaa aaaaaaa 377

10

<210> 38
<211> 1480
<212> DNA
<213> Homo sapiens

15

<400> 38

gcgtaaacac atttttgttc ttagtctatc tcttgtacaa acgatgtgct ttgaagatgt 60

tagtgtataa caattgatgt ttgttttctg tttgatttta aacagagaaa aaataaaaagg 120

20 gggtaatagc tccttttttc ttctttcttt gatttttaac agagaaaaaa taaaaggggg 180

taatagctcc ttttttcttc tttctttttt ttttttcatt tcaaaattgc tgccagtgtt 240

ttcaatgatg gacaacagag ggatatgctg tagagtgttt tattgcctag ttgacaaagc 300

25 tgctttgaat gctgggtggt ctattccttt gacactacgc actttttataa tacatgttaa 360

tgctatagga caagatgctc tgattcctga gtgccagagg ttcaattcag tgtatataac 420

30 tgaacacact catccatttg tgcttttggt ttttttatgg tggcttaaag gtaaagagcc 480

catcctttgc aagtcatcca tgttggtact taggcatttt atcttggtc aaattgttgg 540

aagaatggtg gcttggttca tggtttttgt atttgtgtct aatgcacgtt ttaacatgat 600

35 agacgcaatg catttgttag ctagttttct ggaaaagtca actcttttag gaattgtttt 660

tcagatcttc aataaatttt ttcttttaaat ttcaaagaac aatgtgcttg tgttgatgcc 720

ttacaaaaac cattgtatat ttgtgtatct cttcttgtag ttagacagtg gtttttcagg 780

40 tgcgtgcttt gttttctggt atggccttta tggaatgaga cgcttttagct ttggtacgta 840

gcgctaatac atagcagctt tggcagtttc gtgtcttgag tcttagctaa aaagttagaa 900

gtttacatga ctgttttttt tattttccct aaattattac ttactctgag cattaattaa 960

45 gggcattttc acctgtgtaa aattatgggc agcttttttc tgtctataat tgtttacttt 1020

tgtgggttta ctctagaaac atgagccaaa aatgtcaata gacaacacag tattaaaata 1080

50 acccaaaagt tgtaaagggc aacgtttctc ccctttgata gggacactaa agtgggtctgt 1140

acttgggtag aggatggcag acgttaagaa ttaaaatgcg tctgggtgcg gtctcacgct 1200

tgtaatccca gcactttggg aggctgaggc gggcggatca cctgagggtca ggagttcgac 1260

55 accagcctga tgaacatgga gaaaccccat ctctactaaa aatacaaata ttagctgggc 1320

EP 1 564 293 A1

gttgctgcgc gcctgtaatc ccagcggctc acgaggctga ggcaggagaa ttgcttgagc 1380

tcgggatggc ggaggttgca gtgagccagg attgtgccat tgcactccag cctgggcaac 1440

5 aagagtgaac ctctgtctca aaaaaaaaaa aaaaaaaaaa 1480

<210> 39

<211> 381

10 <212> DNA

<213> Homo sapiens

<400> 39

ttgggtgagg tggaatgatg gtctgttgga atcggtttgg taaatgggtt tatttcatat 60

15 ccgctatctt taacttttga ccgcgttata tatatcatgg cgttcctttc tactttttta

tattggttcg tattatatcg ttctgtattg gggatatgga agacgtatta cttaatgtga 180

ctttattgaa acgttcctct cggtttcgat tctggggggt ttggtctgct cgatggattc 240

20 ttgtcgattt tctcgtgtgg cagtaacata ccgttttata acccttctaa atatcccatc 300

tcccgtgttt tggtaggctc ggaacactat cgaccaacag gttctatcta gaatcaagtt 360

ggaaattaaa cgggtgtcttg g 381

25

<210> 40

<211> 122

<212> PRT

30 <213> Homo sapiens

<400> 40

Met Met Val Cys Trp Asn Arg Phe Gly Lys Trp Val Tyr Phe Ile Ser

1 5 10 15

35 Ala Ile Phe Asn Phe Gly Pro Arg Tyr Leu Tyr His Gly Val Pro Phe

20 25 30

40 Tyr Phe Leu Ile Leu Val Arg Ile Ile Ser Phe Leu Ile Gly Asp Met

35 40 45

Glu Asp Val Leu Leu Asn Cys Thr Leu Leu Lys Arg Ser Ser Arg Phe

50 55 60

45 Arg Phe Trp Gly Ala Leu Val Cys Ser Met Asp Ser Cys Arg Phe Ser

65 70 75 80

50 Arg Val Ala Val Thr Tyr Arg Phe Ile Thr Leu Leu Asn Ile Pro Ser

85 90 95

Pro Ala Val Trp Met Ala Arg Asn Thr Ile Asp Gln Gln Val Leu Ser

100 105 110

55

EP 1 564 293 A1

Arg Ile Lys Leu Glu Ile Lys Arg Cys Leu
115 120

5

<210> 41
<211> 420
<212> DNA
<213> Homo sapiens

10

<400> 41
cccacaggtc ctaaactacc aaacctgcat taaaaaattt cggttgggtcg acctcggagc 60
agaacccaac ctccgagcag tacatgctaa gacttcacca gtcaaagcga acgtactata 120
ctcaattgat ccaataactt gaccaacgga acaagttacc ctagggataa cagcgcaatc 180
cgatgggtgca gccgctatta aaggttcgtt tgttcaaacg attaaagtcc tcgtgtctga 240
gttcagaccg aagtaatcca ggtcgggtttc tatcttcttc aaattcctcc ctgtaccgaa 300
aggactaatg agaaataagg cctacttcac aaagcggcct tccccgtaa tgatatcatc 360
tcaacttagt attataccca caccacacca agaacagggtt tgtaaaaaa aaaaaaaaaa 420

25

<210> 42
<211> 381
<212> DNA
<213> Homo sapiens

30

<400> 42
aaccactcc accttactac cagacaacct tagccaaacc atttaccxaa ataaagtata 60
ggcgatagaa attgaaacct ggcgcaatag atatagtacc gcaaggaaag atgaaaaatt 120
ataaccaagc ataatatagc aaggactaac ccctatacct tctgcataat gaattaacat 180
gaaataactt tgcaaggaga gccaaagcta agacccccga aaccagacga gctacctaag 240
aacagctaaa agagcacacc gtcattgtat ggcaaaatag tgggaagatt tatagggtag 300
agggcgacaa accatccgag ccttgtgata gctgggtgtc caagatagat cttagttcaa 360
cctttaattt gccacagaac c 381

40

<210> 43
<211> 629
<212> DNA
<213> Homo sapiens

45

<400> 43
tttttttttt tttttaacaa accctgttct tgggtgggtg tgggtataat actaagttga 60
gatgatatca ttacggggga aggccgcttt gtgaagtagg ccttatttct cattagtcct 120
ttcggtagag ggaggaattt gaagaagata gaaaccgacc tggattactt cggctctgaac 180
tcagacacga ggactttaat cgtttgaaca aacgaacctt taatagcggc tgcaccatcg 240

55

EP 1 564 293 A1

	ggatgtcctg atccaacatc gaggtcgtaa accctattgt tgatatggac tctagaatag	300
5	gattgcgctg ttatccctag ggtaacttgt tccgttggtc aagttattgg atcaattgag	360
	tttagtagtc cgcttggagt ggtgaagtct agaatgtcct gttcgggggt tggtttctgc	420
	tcccaggtcg ccccaaccga attttttatt gaaggttggg tagtttagca cctgtggggt	480
10	ggtaaggtac tgttggaatt aataaattaa agctccatag ggtctcctcg tcttgttgtg	540
	taatgcccc ctctccacgg gaaggtcaat tccactgggt aaaagtaaga gaaagctgaa	600
	ccctcgggga gccatccata caggtcccc	629
15	<210> 44 <211> 256 <212> DNA <213> Homo sapiens	
20	<400> 44 gcgggtaaat tggtttggtt ttttttaaaa aaaacttgca tgtttaaaaa aaagttgatt	60
	gcttcaaatt tctgctacta acttcaagct atgggagttt ggcagtagtc acttgaggat	120
25	tttttttcca attcttttct ttttgttgtt aaagctgtac ttcagtgaac agaaaaattg	180
	ccaagcaaac taatggacta taaagcgtaa tttgactgtg tgggactaaa ctacagagcc	240
	tacttgacca gtggat	256
30	<210> 45 <211> 270 <212> DNA <213> Homo sapiens	
35	<400> 45 catgtttaaa aaaaagttga ttgcttcaaa ttactgctac taacttcaag ctatgggagt	60
	ttggcagtag tcacttgagg attttttttc caattcgttt tcatttttgt tgttaaagct	120
40	cgtacttcag tgagacagaa aaattgccaa gctaaactaa tgggtctataa aagcgtaatt	180
	tgcattgtgtg ggcaaaaact acagagcctc aattgccact gaggtatagt acaaagtttt	240
	aatacatttt gttaatcaaa ttgaaagaaa	270
45	<210> 46 <211> 270 <212> DNA <213> Homo sapiens	
50	<400> 46 catgtttaaa aaaaagttga ttgcttcaaa ttactgctac taacttcaag ctatgggagt	60
	ttggcagtag tcacttgagg attttttttc caattcgttt tcatttttgt tgttaaagct	120
55	cgtacttcag tgagacagaa aaattgccaa gctaaactaa tgggtctataa aagcgtaatt	180

EP 1 564 293 A1

tgcattgtgtg ggcaaaaact acagagcctc aattgccact gaggtatagt acaaagtttt 240
 aatacatttt gtaaatcaaa ttgaaagaaa 270
 5
 <210> 47
 <211> 184
 <212> DNA
 <213> Homo sapiens
 10
 <400> 47
 tctgcccagg ctggtctgaa attcctgggc tgaagtgatc ctccagtctt ggcctcccaa 60
 agtgctggga ttacaggcat gagctactga gcctagcctt aatgattaat tttagagtga 120
 15
 tggcttgtag cttcaagaca catatagatt gagacagaaa atttccatcg tccccgagaa 180
 aact 184
 20
 <210> 48
 <211> 75
 <212> PRT
 <213> Homo sapiens
 25
 <400> 48
 Ser Ser Ser Leu Gly Leu Pro Lys Cys Trp Asp Tyr Arg His Glu Leu
 1 5 10 15
 30
 Leu Ser Leu Ala Leu Met Ile Asn Phe Arg Val Met Ala Cys Thr Phe
 20 25 30
 Lys Gln His Ile Glu Leu Arg Gln Lys Ile Ser Ile Val Pro Arg Lys
 35 35 40 45
 35
 Leu Cys Cys Met Gly Pro Val Cys Pro Val Lys Ile Ala Leu Leu Thr
 50 55 60
 40
 Ile Asn Gly His Cys Thr Trp Leu Pro Ala Ser
 65 70 75
 45
 <210> 49
 <211> 1381
 <212> DNA
 <213> Homo sapiens
 <400> 49
 50
 tttttttttt gagatggagt tttcgtcttt gttgcccagg ctggagtgca atggcgcaat 60
 ctcagctcac cgcaacctcc gcctcccggg ttcaagcgat tctcctgcct cagcctcccc 120
 agtagctggg attacaggca tgtgcaccac gctcggctaa ttttgtattt ttttttagta 180
 55
 gagatggagt ttaactccat gttggtcagg ctggtctcga actcccgacc tcagatgatc 240

EP 1 564 293 A1

	tcccgtctcg	gcctgccc	aa agtgctgaga	ttacaggcat	gagccac	cat gcccggcctc	300	
	tgcttg	gcta atttttgtgg	tagaaacagg	gtttcactga	tgttgcc	caa gctgggtctcc	360	
5	tgagctcaag	cagtc	ccctcagcct	cccaaagtgc	tgggattaca	ggcgtcagcc	420	
	gtgcctggcc	tttttat	tttttttt	agacacaggt	gtaccactct	taccaggat	480	
10	gaagtgcagt	ggtgtgatca	cagctcactg	cagccttcaa	ctcctgagat	caagcaatcc	540	
	tcctgcctca	gcctcccaag	tagctgggac	caaagacatg	caccactaca	cctggtaatt	600	
	tttat	tttttaattt	tttgagacag	agtctcactc	tgtcacc	cag gctggagtg	660	
15	agtggcgcaa	tcttggtca	ctgcaacctc	tgctcccg	gttcaagtta	ttctcctgcc	720	
	ccagcctcct	gagtagctgg	gactacaggc	gccaccacg	cctagcta	at tttttgtat	780	
	ttttagtaga	gatgggggtt	caccatgttc	gccaggtga	tcttgatctc	ttgacctgt	840	
20	gatctgcctg	cctcggccta	cccaaagtgc	tgggattaca	ggtcgtgact	ccacgccggc	900	
	ctat	tttttaa	ttttgtttg	tttgaaatgg	aatctcactc	tgttacc	cag gtcggagtg	960
	aatggcaa	at ctcggctact	cgcaacctct	gcctcccg	g tcaagcgatt	ctcctgtctc	1020	
25	agcctcccaa	gcagctggga	ttacgggacc	tgcaaccac	cccgtata	att tttgtatttt	1080	
	cattagaggc	gggtttacca	tatttgtcag	gctgggtctc	aaactcctga	cctcagg	tga 1140	
	cccacctgcc	tcagccttc	aaagtgtctg	gattacaggc	gtgagccacc	tcaccagcc	1200	
30	ggctaatttg	gaataaaaa	tatgtagcaa	tgggggtctg	ctatgttgcc	caggctgg	1260	
	tcaaacttct	ggcttcagtc	aatccttcca	aatgagccac	aacacc	cagc	acatt 1320	
	ttttaaacag	ttacatcttt	attttagtat	actagaaagt	aatacaataa	acatgtcaaa	1380	
35	c						1381	
	<210> 50							
	<211> 2520							
40	<212> DNA							
	<213> Homo sapiens							
	<400> 50							
	ccattgttag	gttgtctctt	acctgttaaa	atcaggagct	gacaagaa	at gcttaccaca	60	
45	aaaggagaaa	tgccagtcta	gttaacagtc	aaggagagaa	atcaggaaga	ttatgtgggt	120	
	ggaagaagta	gatgatgtgg	ctgatgagtg	agtgagtgag	caagcctccg	cccagctgaa	180	
	gaaggagtca	gaactgccct	ttgttcccaa	ctat	ttggcg aaccccagcc	ttccctttta	240	
50	tctatacacc	cacagcagag	gattcagccc	agatgcagaa	tgggggcccc	tccacacccc	300	
	ctgcacaccc	ccctgcagat	ggctcacctc	cattgtcttc	ccctgggaac	ctccctgtt	360	
55	agggaccttt	ccccgggacc	acacctcttt	ggcactagtt	cagaatgg	tg atgtgtcggc	420	

EP 1 564 293 A1

	ccctctgcca tactagaaca ccagaaagac aaacgggtga tgtttgtcag ctacagtgag	480
5	tctagagccg tcttgttttc ttctgtcccg tcccaagcca ccatgtctct tcgagcctca	540
	aaatgggacg tatgcaggac cagcgcccag attccaagcc atttttcttc actggagcat	600
	ttccatttaa tatgcaagag ctggtactca aggtgagaat tcagaacca tctcttcgag	660
10	aaaatgattt cattgaaatt gaactggacc gacagagctc acctaccaag agttgctcag	720
	agtgtgttgc tgtgagctgg gtgttaatcc agatcaagtg gagaagatca gaaagttacc	780
	caatactctg ttaaggaagg acaaggatgt tgctcgactc aagatttcag gagctggaac	840
15	tggttctgat gatagtgaat ataattttct gttcagaaat gctgcatcac actgactgaa	900
	aggccttgct atacaggaga gcttcaaaac tgacttacta atgcagcagg gacttttata	960
	ctgagtatat gacagtgtgc atcacctctg ggccaaggac aagccatgat ctaaagcct	1020
20	cagatgcccg ggccagtctg gtgcactgca tagtatatac gaacatcatt ctgccaagg	1080
	taggaagccc catgaccccc aagcagtggg gtccactctt ccaagcctct tgggtgcacaa	1140
	taaaccttat tgcttgaagc tttgaacgac tgtgagaatg gtctggcgag gacgagaacg	1200
25	tgggaattata tgagtgtctt ttgtatccga gaatgtagag agttctctga agacgacgac	1260
	tgagagagag cggacgctat ttctagccac tctgttgac agtgcacctg aagggtctggg	1320
30	atgcgttttt cttggtgttg catgctcaca actctgctga cattgggaac ttatgagaga	1380
	ggaagactcg ggaaagcaca gatactggac agatggattc tgggtgtgggg aaagcacaga	1440
	tactggacag atggttctag tgtgacttgt gactgtgagg tttcctataa catatttata	1500
35	aatgttcacg aggttcaaaa gtctataaga atacagtctg agactgaatt gcttcgaaat	1560
	acttcgatgt tgggaaccaa aagagctttc cctccctcac tttttccttt gtaacactca	1620
	tgactgcttc tctgtctcga gtcactctct cattaaactc ccttcgtggg cactagaggg	1680
40	ctctctgatg cttctaagac actgcttttt acatgccaca cccaccgct agagacaggg	1740
	tctcactatg tggcccaggc tgggtctcaa cttctggcct taagtgatcg tcctgtcctt	1800
	cgcgctcgga agaaagtcgt ggggattaca ggtgtgagcc acccgcccag cccctccctt	1860
45	gtgtttcaac caatcggaag tgaatttaac tagatgtagt aacctttttt ttctttgact	1920
	tctaaaaaag ttacagttta ctaataaagt taagtctggt tctgtcctag aggaaataaa	1980
	ttcactatta attcatgtct taagttactt ggggttaaaac actttcagcc acccagatta	2040
50	attaaagtgg agcagtggag cccctggctg gggagatggg cctccagagg agcagctgca	2100
	ggcatgttct ggctacacag aggcaagcaa gggactggtg tctctggtga gaggtggggt	2160
55	tgatgtatct ctgtcctatg ctggtctctc ttctccttta taaatcctcc tgtggtcact	2220

EP 1 564 293 A1

gactatcgtgta tcgcagtgat cagactgcac atagtagcgt taggctgagc ttaatgtctt 2280

aatcatgtca ttcgagagaa gacacgtttt gattcatgct ttgtgtaatt aatcaatcaa 2340

5 ggattctttt tttagctttg ttgacgtgta attcaccctt cctcctccac tgcataattta 2400

aagcatgtgt tcacactgtg tgtatacatt cactgctgatt ttttcgtttg ctgcattgct 2460

10 tggactgttc ataacatcac aagtattatt caaataaaat attaactgac cgaaaaaaaa 2520

<210> 51
<211> 141
<212> DNA
15 <213> Homo sapiens

<400> 51
gaattcctgg gctcaagtga tcctctcatg tcagtctccc aaagtgctgg gatgacaggc 60

ttgagccacc acaccaggcc catcatcagt ttttatataa agaaaaaaaa accttaaaat 120

20 tgttagcaaa atactatgac a 141

<210> 52
<211> 151
25 <212> DNA
<213> Homo sapiens

<220>
30 <221> misc_feature
<222> (96)..(96)
<223> n is a, c, g, or t

<400> 52
gaactcctga cctcaggtga tccgcccgcc tcagcctccc aaagtgctgg gattacaagc 60

35 gtgcagaccg caccagagcg attttaattc ttaacntgcc atcctctacc caagtacaga 120

ccactttagt gtccctatca aaggggagac a 151

40 <210> 53
<211> 43
<212> DNA
<213> Homo sapiens

<400> 53
45 aattctcctg cctcagcctc gtgagccgct gggattacag gcg 43

<210> 54
<211> 45
50 <212> DNA
<213> Homo sapiens

<400> 54
aagccaactc agactcagcc aacaggtaag tgggcattac aggag 45

55

EP 1 564 293 A1

<210> 55
 <211> 143
 <212> DNA
 5 <213> Rattus sp.

 <400> 55
 ctcagttttc actttgatct ggtagatagt tttcgtttca gttgggggag aaggatctgt 60
 ttgtaagaac ggagtgacgg gataccataa aaatagaggt aataacatac attgggacgt 120
 10 gtaaatttat ttttatggaa gtg 143

 <210> 56
 <211> 157
 <212> DNA
 15 <213> Homo sapiens

 <400> 56
 ctcacagttt ccttatcttg gtggtcgtaa gttttcgtcg aaacagttga tcgttatttg 60
 20 tgagattgtc gtatagggag actaacaggt agtaactttt gtgaccgtcg ttaaaacttt 120
 actttttttt ttctttcttc ttttttcctt cataatg 157

 <210> 57
 <211> 60
 <212> DNA
 25 <213> Homo sapiens

 <400> 57
 30 accacgcccc gctaattttt gtatttttag tagagacagg gtttcaccgt gttggccagg 60

 <210> 58
 <211> 60
 <212> DNA
 35 <213> Homo sapiens

 <400> 58
 acaacgcccc gctaatatat gtatttttag tagagatggg gtttctccat gttcatcagg 60
 40
 <210> 59
 <211> 60
 <212> DNA
 <213> Homo sapiens
 45
 <400> 59
 ctggtctgaa attcctgggc tgaagtgatc ctccagtctt ggccctccaa agtgctggga 60

 <210> 60
 <211> 60
 <212> DNA
 50 <213> Homo sapiens

 <400> 60
 55 ctggtgtcga actcctgacc tcaggtgatc cgcccgctc agcctccaa agtgctggga 60

EP 1 564 293 A1

	<210> 61	
	<211> 26	
	<212> DNA	
5	<213> Homo sapiens	
	<400> 61	
	agacacatat agattgagac agaaaa	26
10	<210> 62	
	<211> 30	
	<212> DNA	
	<213> Homo sapiens	
15	<400> 62	
	agtacagacc acttttagtgt ccctatcaaa	30
20	<210> 63	
	<211> 31	
	<212> DNA	
	<213> Homo sapiens	
	<400> 63	
	agatctcgct ctgtcaccca ggctgaagtg c	31
25	<210> 64	
	<211> 34	
	<212> DNA	
	<213> Homo sapiens	
30	<400> 64	
	agagtttcac tcttgcttgc ccaggctgga gtgc	34
35	<210> 65	
	<211> 59	
	<212> DNA	
	<213> Homo sapiens	
40	<400> 65	
	agtggcccaa tctcggtca ctgcgagctc cacctcccgg gttcacttca ttctcctgc	59
45	<210> 66	
	<211> 60	
	<212> DNA	
	<213> Homo sapiens	
	<400> 66	
	aatggcaciaa tcctgggtca ctgcaacctc cgccctcccg agctcaagaa cttctcctgc	60
50	<210> 67	
	<211> 66	
	<212> DNA	
	<213> Homo sapiens	
55	<400> 67	

EP 1 564 293 A1

	ctcagcctct gagtagctgg gactacaggc gccaccaca agccgctaatt ttttgtattt	60
	ttgtag	66
5		
	<210> 68	
	<211> 67	
	<212> DNA	
	<213> Homo sapiens	
10		
	<400> 68	
	ctcagcctcg tgagccgctg ggattacagg cgcgcgccac aagcgactaa ttttgtatt	60
	tttgtag	67
15		
	<210> 69	
	<211> 76	
	<212> DNA	
	<213> Homo sapiens	
20		
	<400> 69	
	accacgcccc gctaattttt gtatttttag tagagacagg gtttcaccgt gttggccagg	60
	atgctcgatc tcctga	76
25		
	<210> 70	
	<211> 78	
	<212> DNA	
	<213> Homo sapiens	
30		
	<400> 70	
	acaacgcccc gctaattttt gtatttttag tagagatggg gtttctccat gttcatcagg	60
	ctgggtgctga actcctga	78
35		
	<210> 71	
	<211> 159	
	<212> DNA	
	<213> Homo sapiens	
40		
	<400> 71	
	ccccaagcag tgtaaatcct ggctactgtg tgagctgacc tcaagcacag gtgaaggcag	60
	agaatccatc cacctgtttc tgttctccct gcttagctcc agggatggaa ctgggactgg	120
	gatagaggaa aggtgaactc ctcattaagg aatggatg	159
45		
	<210> 72	
	<211> 170	
	<212> DNA	
	<213> Homo sapiens	
50		
	<400> 72	
	cccctgttct tgggtggggt tgggtatatt ctggttgaga tgatatcatt tacgggggaa	60
	ggcgctttgt gaagtaggcc ttatttctct tgtcctttcg tacagggagg atttgaagta	120
55		

EP 1 564 293 A1

gtagaacgct gttactccgg tctgaactca gtcacgtggc tttatcgttg 170

5 <210> 73
<211> 52
<212> DNA
<213> Homo sapiens

10 <400> 73
gatccaagct acgtacgcgt gcatgcacgt catagctctt ctatagtgtc ac 52

15 <210> 74
<211> 53
<212> DNA
<213> Homo sapiens

<400> 74
gatccgagct cggtaccaag ttgatgcata gcttgagtat tctatagtgt cac 53

20 <210> 75
<211> 115
<212> DNA
<213> Homo sapiens

25 <400> 75
gtatggggcc gatagcttat ttagccttta gagcacactg gcggccgtta ctagtggatc 60
cgagctcggg accaacttga tgcatagctt gagtattcta tagtgtcacc taaat 115

30 <210> 76
<211> 120
<212> DNA
<213> Homo sapiens

35 <400> 76
atatagacaa tataacaata tattgtatac ttagagcac actggcagcc gttactagtg 60
gatccgagct cggtaccaag ttgatgcata gcttgagtat tctatagtgt cactaatagt 120

40 <210> 77
<211> 117
<212> DNA
<213> Homo sapiens

45 <400> 77
cttaatagat agctacttaa aataacttac acactgtttt agagtgcctg aaaactatct 60
gatcagacat agtattgaaa ccaatgaata cattatataa agtaaaggaa aggagaa 117

50 <210> 78
<211> 137
<212> DNA
<213> Homo sapiens

55 <400> 78
cttactacca gacaacctta gccaaaccat ttacccaaat aaagtatagg cgatagaaat 60

EP 1 564 293 A1

	tgaaacctgg cgcaatagat atagtaccgc aaggaaagat gaaaaattat aaccaagcat	120
	aatatagcaa ggactaa	137
5		
	<210> 79	
	<211> 198	
	<212> DNA	
	<213> Homo sapiens	
10		
	<400> 79	
	ctataaaggt cgttgtaaac gataaagcac gtgactgagt tcagaccgga gtaacagcgt	60
	tctactactt caaatcctcc ctgcgaaagg caagagaaat aaggcctact taagcgctt	120
15		
	ccccgtaaa tgatatcatc tcaaccagaa tatacccaaa cccccaaga acaggggagg	180
	aaaagaaaaa aaaaaaaa	198
20		
	<210> 80	
	<211> 200	
	<212> DNA	
	<213> Homo sapiens	
25		
	<400> 80	
	ctatagagat tgttgatctg cctcttaagc aagagattca ttgcagctca gcatggctca	60
	gaccagctca tacttcatgc tgatctcctg cctgatgttt ctgtctcaga gccaaggtaa	120
	gatctctttt ccaactcttt ctagccctga agacttcact ctatcccaa gcatacgggt	180
30		
	ctacttgaaa aaaaaaaaaa	200
35		
	<210> 81	
	<211> 82	
	<212> DNA	
	<213> Homo sapiens	
40		
	<400> 81	
	cagaaaacta gctacacaat gcattggctc atcatgttaa aacgtgcatt agacacaaat	60
	acaaaaacca tgaaacaagc ca	82
45		
	<210> 82	
	<211> 90	
	<212> DNA	
	<213> Homo sapiens	
50		
	<400> 82	
	cagaaaaatt gccaagctaa actaatggtc tataaaagcg taatttgcat gtgtgggcat	60
	aaactacaga gctcatgcta gagtatgcaa	90
55		
	<210> 83	
	<211> 141	
	<212> DNA	

EP 1 564 293 A1

<213> Homo sapiens

<400> 83
5 aattgggtac cgggcccccc ctagaggtcg acggtatcga taagcttgta tcgaattccg 60
gactttgctt ttggttttcc tttcctgtga aaagggttgg tttaaagtga gatacacttt 120
tccgtagaac aagtgttcta t 141

10 <210> 84
<211> 155
<212> DNA
<213> Homo sapiens

15 <400> 84
aagttgattg cttcaaattt ctgctactaa cttcaagcta tgggagtttg gcagtagtca 60
cttgaggatt ttttttccaa ttcgttttca tttttgttgt taaagctcgt acttcagtga 120
20 gacagaaaaa ttgccaaagct aaactaatgg tctat 155

<210> 85
<211> 232
<212> DNA
25 <213> Homo sapiens

<400> 85
gaattcctgg gctcaagtga tcctctcatg tcagtctccc aaagtgctgg gatgacaggc 60
30 ttgagccacc acaccagccc atcatcagtt tttatataaa gaaaaaaaaa ccttaaaatt 120
gttaggcaaa taatgacaaa ttgtaataata tattcttaca tttcagattt ttatttttta 180
aactgataag aattgattaa taaataaaat ttagtattaa tctgtctttt aa 232

35 <210> 86
<211> 245
<212> DNA
<213> Homo sapiens

40 <400> 86
aaattcctgg gctgaagtga tcctccagtc ttggcctccc aaagtgctgg gattacaggc 60
atgagctact gagcctagcc ttaatgatta attttagagt gatggcttgt accttcaagc 120
45 aacatataga gttgagacag aaaattttcca tcgtcccagag aaaactgtgc tgcattgggcc 180
ccgtgtgccc tgtgaagatc gccctattaa ctataaatgg gcattgcaca tggttgccag 240
cttca 245

50 <210> 87
<211> 239
<212> DNA
<213> Homo sapiens

55 <400> 87

EP 1 564 293 A1

	aacgtttcga acctatcgtg aagccccgatt ttagagttaa tacgggtgct tcaaggaac	60
	ggggctatga gaagttttct acggggagca tggaaatctt ctgtctcaat atgtgcttga	120
5	aggtacaacc gtatctaaaa ttaatcatta aggctaggct cagtagctct gcctgtaac	180
	ccagcacttt cgggaggcca agactggagg atcacttcag cccaggaatt tcagacgcc	239
10	<210> 88 <211> 260 <212> DNA <213> Homo sapiens	
15	<400> 88 tactgtgtga gcctgacctc aagcacagga ttccagaaat ggaaggatgt gccttgtgaa	60
	gacaagttct cctttgtctg caagttcaaa aactagaggc agctggaaaa tacatgtcta	120
	gaactgatcc agcaattaca acggagtcaa aaattaaacc ggaccatctc tccaactcaa	180
20	ctcaacctgg acactctctt ctctgctgag ttgacctgt taatcttcaa tagttttacc	240
	tacccagtc tttggaacct	260
25	<210> 89 <211> 149 <212> DNA <213> Homo sapiens	
30	<400> 89 cttgcttgcc caggctggag tgcaatggca caatcctggc tcaactgcaac ctccccctcc	60
	cgagctcaag aacttctcct gcctcagcct cgtgagccgc tgggattaca ggcgcgcgcc	120
	acaagcgact aatatttgta tttttgtag	149
35	<210> 90 <211> 167 <212> DNA <213> Homo sapiens	
40	<400> 90 ctcgctctgt caccaggtc gaagtgcagt ggcccaatct cggctcactg cgagctccac	60
	ctcccggtt cacttcattc tcctgcctca ctgcctcagc ctctgagtag ctgggactac	120
45	aggcgccac caccagtcct cctgctaatt ttttgatatt ttagtag	167
50	<210> 91 <211> 84 <212> DNA <213> Homo sapiens	
	<400> 91 ccatgttcat caggctggtg tcgaactcct gacctcgtga tccgccgcc tcagcctccc	60
55	aaagtgctgg gattacaagc gtgc	84

EP 1 564 293 A1

	<210>	92	
	<211>	85	
	<212>	DNA	
5	<213>	Homo sapiens	
	<400>	92	
	ccgtgttggc caggatgggc tcgatctcct gacctcgtga tccgcccggc ttggccaccc	60	
10	aaagagtttg ggattacagg cgtgc	85	
	<210>	93	
	<211>	251	
	<212>	DNA	
15	<213>	Homo sapiens	
	<400>	93	
	tgcagcaatg gcaacaacgt ctgcaaacta ttaactggcg aactacttac tctagcttcc	60	
20	cggcaacaat taatagactg gatggaggcg gataaagttg caggaccact tctgcgctcg	120	
	gcccttccgg ctggctgggt tattgctgat aaatctggag ccggtcgagc gtgggtctcg	180	
	cgtatcattc gagcactggg gccagatggg aagccctccg tctcgtagtt atctcacagc	240	
25	agggagtcag g	251	
	<210>	94	
	<211>	242	
	<212>	DNA	
30	<213>	Homo sapiens	
	<400>	94	
	tgcaggagcg gggaggcacg atggccgctt tggccggat ctttgtgagg aaccttactt	60	
35	ctgtgggtgtg acataattgg acaaactacc tacagagatt taaagctcta aggaaatata	120	
	aaatttttta gtgtataatg tgttaaacta ctgattctaa ttgtttgtgt attttagatt	180	
	ccaaccctat ggaacctgat gaatgggagc cagtgggtgga atgcctttta tgaggaaacc	240	
40	tg	242	
	<210>	95	
	<211>	208	
	<212>	DNA	
45	<213>	Homo sapiens	
	<400>	95	
	tgcagcaatc tttcttatat acatgcttaa tagatagcta cttaaaataa cttacacacg	60	
50	tttttagagtt gcttgaaaac tatctgatca agacatagta attgaaacca atgaatacat	120	
	tatataaagt aaaggaaagg agaagagagg aaagggaggg gaagaggaga gggagggaca	180	
55	agcgagaaag gaaaggaag ggagaaaa	208	

EP 1 564 293 A1

5 <210> 96
 <211> 152
 <212> DNA
 <213> Homo sapiens

 <400> 96
 ctcactaaag ggatcaagga ataattttga atttcaagtc ttacatttaa taaatacatt 60
 10 cataaggcta taactaccat acgttgtgat ttctctgatt aatttaaaaa taaattaaaa 120
 cctggaaaga attttaccat tctaggaagc ca 152

 15 <210> 97
 <211> 338
 <212> DNA
 <213> Homo sapiens

 20 <400> 97
 aatctatctt atatacatgc ttaatagata gctacttaaa ataacttaca cacgttttag 60
 agttgcttga aaactatctg atcaagacat agtaattgaa accaatgaat acattatata 120
 aagtaaagga aaggagaaga gaggaaagga ggggagagga gaggaggaca agcgagaaaa 180
 25 ggaagggaag ggagaaaaag ggggaaaggg aggtagagag agagagaaaa agtgctggtc 240
 atatagtaag tgtacatctt aactttttta gaaactaccc tactctattc cagagtgatt 300
 gtacatgtgc attttactgc attatagaga tcattttc 338
 30

 35 <210> 98
 <211> 169
 <212> DNA
 <213> Homo sapiens

 <400> 98
 tgcaggagtg gggaggcacg atggccgctt tgggtccgat ctttgtgaag gaaccttact 60
 tctgtgtgtg acataattgg acaaactacc tacagagatt taaacgtcta aggtaaatat 120
 40 aaaattttta gtgtataggt taaactactg attctaattgt tgtgtatctt 169

 45 <210> 99
 <211> 209
 <212> DNA
 <213> Homo sapiens

 <400> 99
 ccccggtctg cagcaatggc aacaacgtct gcaaactatt aactggcgaa ctcatcctc 60
 50 tagcttcccc gcaacaatta atgactggat ggaggcggat aaagttgcag gaccatttct 120
 cgcggtggcc ttccggctgg ctggtttatt gctgataatt gagcgtgcga gtggctcgcg 180
 tatcattcgc gacatgggccc agtaggtac 209
 55

EP 1 564 293 A1

<210> 100
 <211> 272
 <212> DNA
 <213> Homo sapiens

5

<400> 100
 cttgcccttc atggagtcac acagccgac agcaaaatgc aggggcttgt tctgaatgca 60
 ctgaaccagg ttcaggaaag ctttttccag gtctccttta acctctttcc tgatgctttc 120
 10 caacatgtca taagggtgt aactcttgta cctatcaaact actttctgga ggtggggaca 180
 cgctcgctgc ggcatgatg ctgatccact tgggaacatc agttctttcc tcttcactcc 240
 15 agctgcatag agatccgagg actcttggtc aa 272

<210> 101
 <211> 278
 <212> DNA
 <213> Homo sapiens

20

<400> 101
 acggcccagc ttccttcaaa atgtctactg ttcacgaaat cctgtgcaag ctgagcttgg 60
 25 agggatgatc ctctacaccc ccaagtgcac atgggtctgt caaagcctat actaactttg 120
 atgctgagcg ggatgctttg aacattgaaa cagccatcaa gaccaaaggt gtggatgagg 180
 tcaccattgt caacattttg accaaccgca gcaatgacac gagacaggat attgccttcg 240
 30 cctaccagag aaggacaaa aaaggaactt gcatcaca 278

<210> 102
 <211> 228
 <212> DNA
 <213> Homo sapiens

35

<220>
 <221> misc_feature
 <222> (226)..(226)
 <223> n is a, c, g, or t

40

<400> 102
 agcaatagca aaggaaagga aacaatatat agcaagggtt attcttcctt tgtgtcagca 60
 45 tttctgagtg tgcacacagg cccagtgatt ccatgtatct ttgagtgacc actgcctctg 120
 tctggccctt ccccatagaa ccgccgctgg tggagcgtgg gtccctggtc tcctacaagt 180
 50 cctggggcat tggagcccca agcagtgtta atcctggcac tgtgtgac 228

<210> 103
 <211> 246
 <212> DNA
 <213> Homo sapiens

55

EP 1 564 293 A1

```

<220>
<221> misc_feature
<222> (191)..(191)
5 <223> n is a, c, g, or t

<400> 103
agcaatggca acaacgtctg caaactatta actggcgaac tacttactct tagcttccgg 60
10 caacaattaa tagactggat ggaggcggat aaagttgcag gaccacttct gcgctcggcc 120
cttccggctg gctgggtttat tgctgataaa tctggagccg gtcgagcgtg ggtctcgcgt 180
atcattcgag nctggggcca gatggtaagc cctccgtatc gtagttatct cacagcaggg 240
15 agtcag 246

<210> 104
<211> 86
<212> DNA
20 <213> Homo sapiens

<400> 104
ctggcactgg agcagtgggt ccctgggtctc ctacaagtcc tggggcattg gagccccaag 60
25 cagtgttaat cctggcactg tgtgag 86

<210> 105
<211> 154
<212> DNA
30 <213> Homo sapiens

<220>
<221> misc_feature
<222> (40)..(40)
35 <223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (99)..(99)
40 <223> n is a, c, g, or t

<400> 105
ctggagccgg tcgagcgtgg gtctcgcgta tcattcgagn ctggggccag atggtaagcc 60
ctccgtatcg tagttatctc acagccgtat cattcgagnc tggggccaga tggttaagccc 120
45 tccgtatcgt agttatctca cagcagggag tcag 154

<210> 106
<211> 221
<212> DNA
50 <213> Homo sapiens

<400> 106
aggagacttg tggtaaaaat ctgctgctgt actgctcatt tgggaacctt agtatactaa 60
55 ataataaat atatcaacaa ctaatgggtca gccaatgcta tgctggatat gagggctctg 120

```

EP 1 564 293 A1

ggccacaaag acaaaaaatc aggaaccact ttttaagtga gataactttgg gtctctgtca 180
 aattcataac acttatttct tgggtgaata cagttaatga g 221
 5
 <210> 107
 <211> 231
 <212> DNA
 <213> Homo sapiens
 10
 <400> 107
 aggagcgggg aggcacgatg gccgctttgg tccggatctt tgtgaggaac cttacttctg 60
 tgggtgtgaca taattggaca aactacctac agagatttaa agctctaagg aaatataaaa 120
 15
 tttttaagtg tataatgtgt taaactactg attctaattg tttgtgtatt ttagattcca 180
 accctatgga acctgatgaa tgggagccag tgggtggaatg cctttaatga g 231
 20
 <210> 108
 <211> 102
 <212> DNA
 <213> Homo sapiens
 25
 <400> 108
 taaatctgga gccggtcgag cgtgggtctc gcgtatcatt cgagcactgg ggccagatgg 60
 taagccctcc gtatcgtagt tatctcacag cagggagtca gg 102
 30
 <210> 109
 <211> 110
 <212> DNA
 <213> Homo sapiens
 35
 <400> 109
 tagaaccgcc gctggcactg gagcagtggg tccctggtct cctacaagtc ctggggcatt 60
 ggagccccaa gcagtgttaa tcctggctac tgtgtgagcc tgacctcaag 110
 40
 <210> 110
 <211> 85
 <212> DNA
 <213> Homo sapiens
 45
 <400> 110
 atagatatct actttattcg atttaaattc tgttttagtat tttattatat tttgttaatc 60
 catttgtccc aattcatata cttat 85
 50
 <210> 111
 <211> 95
 <212> DNA
 <213> Homo sapiens
 55
 <400> 111
 atagatagct acttaaaata acttacacac tgtttttagag tgcttgaaaa ctatctgac 60

EP 1 564 293 A1

	agacatagta attgaaacca atgaatacat tatat	95
5	<210> 112 <211> 90 <212> DNA <213> Rattus sp.	
10	<220> <221> misc_feature <222> (85)..(86) <223> n is a, c, g, or t	
15	<220> <221> misc_feature <222> (89)..(89) <223> n is a, c, g, or t	
20	<400> 112 gaaggatctg tttgtaagaa cggagcggga taccataaaa atagaggtaa taacatacat tgggacgtgt aaatttattt ttatnnaant	60 90
25	<210> 113 <211> 94 <212> DNA <213> Homo sapiens	
30	<400> 113 gaaggatctt accattttaa gaaagggtcca aaattaaata aaaatttaaat tagtctcttt agtggtgcat accatcaata tcggaatact aaat	60 94
35	<210> 114 <211> 200 <212> DNA <213> Homo sapiens	
40	<400> 114 acctggtgct gtgtcaccc aggccgaggg tgcctttgtg gcctcactga ttaaggagag tggcatgatg acttcaatgt ctggattggc ctccatgacc ccaaaaagaa ccgccgctgg ggagcgtggg tccctgggtct cctacaagtc ctggggcatt ggagcccaa gcagtgttaa tcctggctac tgtgtgagcc	60 120 180 200
45	<210> 115 <211> 218 <212> DNA <213> Homo sapiens	
50	<400> 115 aactggcgaa ctacttactc tagcttccgg caacaattaa tagactggat ggaggcggat aaagttgcag gaccacttct gcgctcggcc cttccggctg gctggtttat tgctgataaa	60 120
55		

EP 1 564 293 A1

	tctggagccg gtgagcgtgg gtctcgcgta tcattgcagc actggggcca gatggtaagc	180
	cctccgtatc gtggttatct acacgacggg gagtacgc	218
5		
	<210> 116	
	<211> 146	
	<212> DNA	
	<213> Homo sapiens	
10		
	<400> 116	
	aggcccatca tcagttttta tataaagaaa aaaaaacctt aaaattgtta ggcaaatact	60
	atgacaaatt gtaatatata ttcttacatt tcagatTTTT attttttaaa ctgtatagaa	120
15		
	ttgattaata aataaaaattt agtatt	146
	<210> 117	
	<211> 155	
20		
	<212> DNA	
	<213> Homo sapiens	
	<400> 117	
	aggcacgatg gccgctttgg tccggatctt tgtgaaggaa ccttacttct gtgtgtgaca	60
25		
	taattggaca aactacctac agagatttaa acgtctaagg taaatataaa attttttagtg	120
	tatagggttaa actactgatt ctaatgttgt gtatt	155
30		
	<210> 118	
	<211> 102	
	<212> DNA	
	<213> Homo sapiens	
	<400> 118	
35		
	taaatctgga gccggtgagc gtgggtctcg cgtatcattg cagcactggg gccagatggt	60
	aagccctccg tatcgtgggtt atctacacga cggggagtagc gg	102
40		
	<210> 119	
	<211> 116	
	<212> DNA	
	<213> Homo sapiens	
	<400> 119	
45		
	tagaacgcc gctggcactg gagcagtggg tccctggtct cctacaagtc ctggggcatt	60
	ggagccccaa gcagtgttaa tcctggctac tgtgtgagcc tgacctcaag cacagg	116
50		
	<210> 120	
	<211> 6	
	<212> PRT	
	<213> Unknown	
	<220>	
55	<223> Unknown Peptide	

<400> 120

His Pro Thr Pro Ala Ala
1 5

<210> 121

<211> 7

<212> PRT

<213> Unknown

<220>

<223> Unknown peptide

<400> 121

Phe Val Ala Ser Leu Ile Lys
1 5

Claims

1. A method for detecting the presence of Neural Thread Protein (NTP) having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, in a human subject, said method comprising:

(a) contacting a biological sample from said human subject that is suspected of containing said NTP with at least one molecule capable of binding to said protein; and

(b) detecting any of said molecule bound to said protein.

2. A method as claimed in claim 1, wherein said molecule is:

(a) an antibody substantially free of natural impurities;

(b) a monoclonal antibody; or

(c) a fragment of (a) or (b).

3. A method as claimed in claim 1 or claim 2, wherein said biological sample is removed from said human subject prior to contacting said sample with said molecule.

4. A method as claimed in any one of claims 1 to 3, wherein the detecting of any of said molecule bound to said protein is performed by in situ imaging.

5. A method as claimed in any one of claims 1 to 4, wherein the detecting of any of said molecule bound to said protein is performed by in vitro or in vivo imaging.

6. A method as claimed in any one of claims 1 to 5, wherein said molecule is administered to said human subject.

7. A method as claimed in any one of claims 1 to 6, wherein said molecule is bound to said protein in *vi vo*.

8. A method of diagnosing the presence of an NTP-related condition in a human subject suspected of having such a condition, which comprises:

(a) incubating a biological sample from said subject which is suspected of containing NTP having a molecular

weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, in the presence of at least one binding molecule capable of identifying said NTP; and

(b) detecting said binding molecule which is bound in said sample, wherein said detection indicates that said subject has an NTP-related condition;

wherein said NTP-related condition is Alzheimer's Disease, the presence of neuroectodermal tumors, the presence of a malignant astrocytoma or the presence of glioblastomas.

9. A diagnostic method as claimed in claim 8, wherein said detection is by immunometric assay.

10. A diagnostic method as claimed in claim 9, wherein said immunometric assay is a monoclonal antibody-based immunometric assay.

11. A diagnostic method as claimed in claim 8, wherein said method comprises:

(a) incubating said biological sample with two different NTP monoclonal antibodies bound to a solid phase support; and

(b) detecting NTP bound to said monoclonal antibodies with a third different detectably labelled NTP monoclonal antibody solution.

12. A diagnostic method as claimed in any one of claims 8 to 11, wherein said incubating step further includes adding a known quantity of labelled Neural Thread Protein wherein a competitive immunoassay is established.

13. A diagnostic method as claimed in claim 12, wherein said label is capable of emitting radiation.

14. A diagnostic method as claimed in claim 13, wherein said label is ¹²⁵I.

15. A diagnostic method as claimed in any one of claims 8 to 16, wherein said detection is by immuno-polymerase chain reaction.

16. NTP substantially free of any natural impurities and having a molecular weight of about 42 kDa, about 26 kDa, about 21 kDa, about 17 kDa, about 14 kDa or about 8 kDa.

17. A recombinant DNA molecule comprising a genetic sequence coding for an NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa.

18. A DNA molecule as claimed in claim 17, wherein said NTP is human NTP.

19. A DNA molecule as claimed in claim 17 or claim 18 which is a plasmid.

20. A host transformed with a plasmid as claimed in claim 19.

21. A method of using a plasmid as defined in claim 19 to prepare an NTP, said method comprising:

(a) introducing said plasmid into a host cell to produce a recombinant host cell;

(b) culturing said recombinant host cell; and

(c) isolating said NTP from said recombinant host cell.

22. A DNA probe comprising a detectably labelled genetic sequence coding for an NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, or a fragment thereof.

23. A method of detecting the presence of a genetic sequence coding for NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa, in a clinical sample, which comprises:

(a) contacting said sample with a probe as defined in claim 27 under conditions of hybridisation; and

(b) detecting the formation of a hybrid of said probe and said sequence.

24. A method of producing an NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa, said method comprising:

(a) culturing a recombinant host comprising a human gene coding for said NTP; and

(b) isolating said NTP from said host.

25. A method as claimed in claim 24, wherein said gene is obtained from brain tissue of a patient with Alzheimer's Disease, or from a human neural tumor cell line.

26. A method as claimed in claim 24 or claim 25, wherein said gene codes for an NTP having a molecular weight of about 42 kDa, about 26 kDa, about 21 kDa, about 17 kDa, about 14 kDa or about 8 kDa.

27. A method as claimed in any one of claims 24 to 26, wherein said host is *E. coli*.

28. A method as claimed in any one of claims 24 to 27, wherein said gene is contained by a vector.

29. A method as claimed in any one of claims 24 to 28, wherein said gene is under control of an inducible promoter.

30. A method as claimed in claim 29, wherein said promoter is a lambda P_L promoter, or a tac promoter.

31. A substantially pure NTP having a molecular weight of about 42 kDa, about 26 kDa, about 21 kDa, about 17 kDa, about 14 kDa or about 8 kDa, obtained by a process as claimed in any one of claims 24 to 30.

32. A 15- to 30-mer antisense oligonucleotide which is complementary to an NTP nucleic acid sequence and which is non-homologous to the PTP nucleic acid sequence.

33. An antisense oligonucleotide as claimed in claim 32 which is DNA.

34. An antisense oligonucleotide as claimed in claim 32 or claim 33 which is an o-oligonucleotide.

35. An antisense oligonucleotide as claimed in claim 32 or claim 33 which is an S-oligonucleotide.

36. A pharmaceutical composition comprising at least one 15- to 30-mer antisense oligonucleotide which is complementary to an NTP sequence and which is non-homologous to the PTP sequence; and a pharmaceutically acceptable carrier.

37. A ribozyme comprising a target sequence which is complementary to an NTP sequence and non-homologous to the PTP nucleic acid sequence.

38. A DNA molecule which codes for a ribozyme as claimed in claim 37.

39. A pharmaceutical composition comprising an NTP ribozyme as claimed in claim 37 and a pharmaceutically acceptable carrier.

40. An oligonucleotide comprising the sequence 3'X5-L-5'X3', wherein X comprises an NTP nucleic acid sequence which is non-homologous to the PTP nucleic acid sequence, and wherein L represents an oligonucleotide linkage.

41. An oligonucleotide comprising the sequence 5'X3'L-3'X5', wherein X comprises an NTP nucleic acid sequence which is non-homologous to the PTP nucleic acid sequence, and wherein L represents an oligonucleotide linkage.

42. A ribonucleotide NTP External Guide Sequence comprising:

(a) a 10-15 nucleotide sequence which is complementary to an NTP nucleic acid sequence and which is non-

homologous to the PTP nucleic acid sequence; and

(b) a 3'-NCCA nucleotide sequence, wherein N is a purine.

5 **43.** An NTP External Guide Sequence as claimed in claim 42 which is DNA.

44. An expression vector comprising a DNA molecule as claimed in claim 17 or claim 18.

10 **45.** A virion comprising an expression vector as claimed in claim 44.

46. A method of differentiating between sporadic and familial Alzheimer's Disease in a human subject, said method comprising:

15 (a) obtaining a biological sample from said human subject who is suspected of having Alzheimer's Disease;

(b) purifying DNA from said biological sample; and

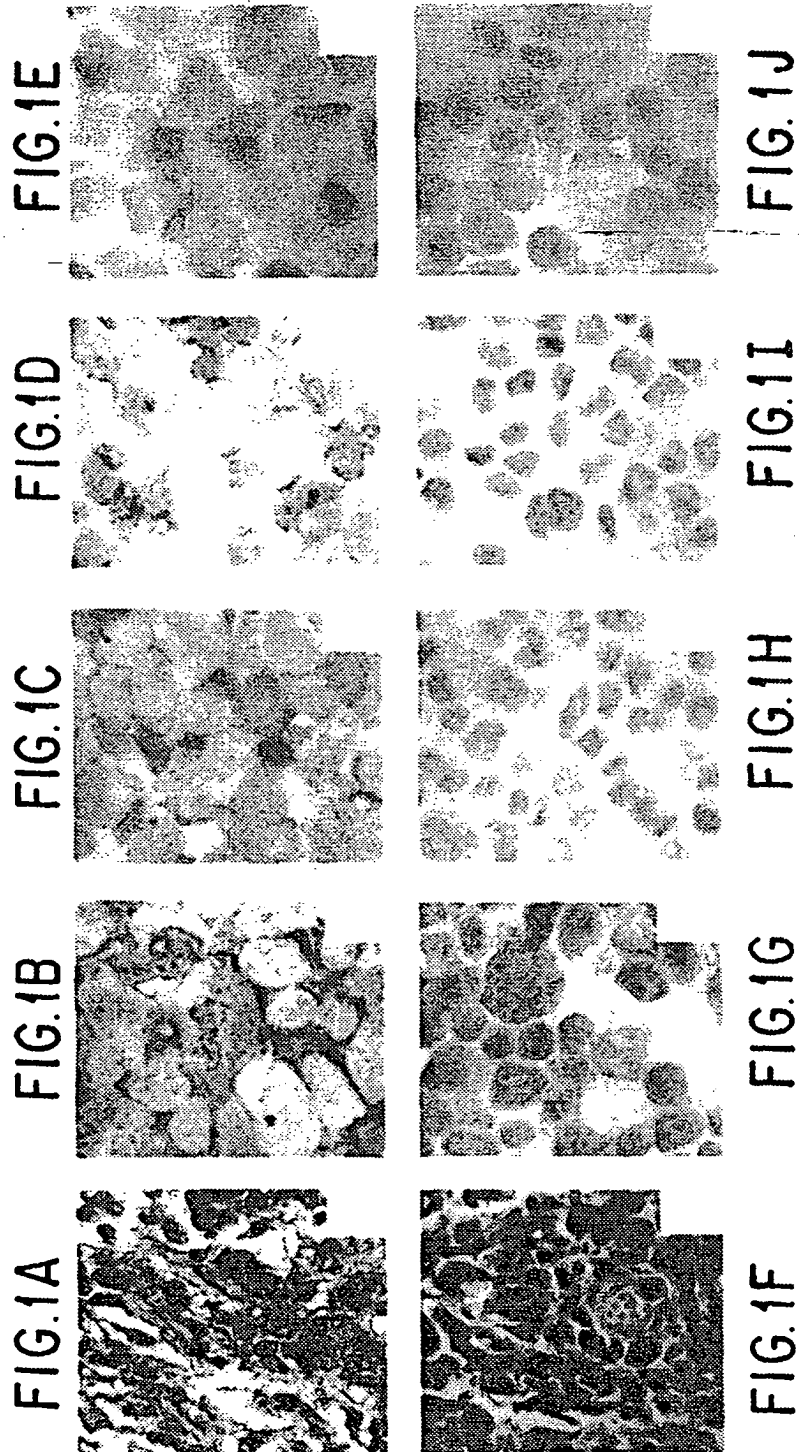
(c) contacting said DNA with a probe as defined in claim 27 under conditions of hybridisation;

20 wherein familial Alzheimer's Disease is indicated by the detection of a hybrid of said probe and said DNA; and wherein sporadic Alzheimer's Disease is indicated by the absence of detection of hybridisation.

47. The use of an antisense oligonucleotide as defined in any one of claims 32 to 35 in the preparation of a medicament for use in inhibiting the expression of an NTP in a patient.

25 **48.** The use of a ribozyme as defined in claim 37 or of a DNA molecule as defined in claim 38 in the preparation of a medicament for use in inhibiting expression of an NTP in a patient.

30 **49.** The use of an oligonucleotide as defined in claim 40 or claim 41, a ribonucleotide NTP External Guide Sequence as defined in claim 42 or claim 43 or a virion as defined in claim 45, in the preparation of a medicament for use in treating a disease or condition mediated by the presence of an NTP having a molecular weight of about 8 kDa, about 14 kDa, about 17 kDa, about 21 kDa, about 26 kDa or about 42 kDa.



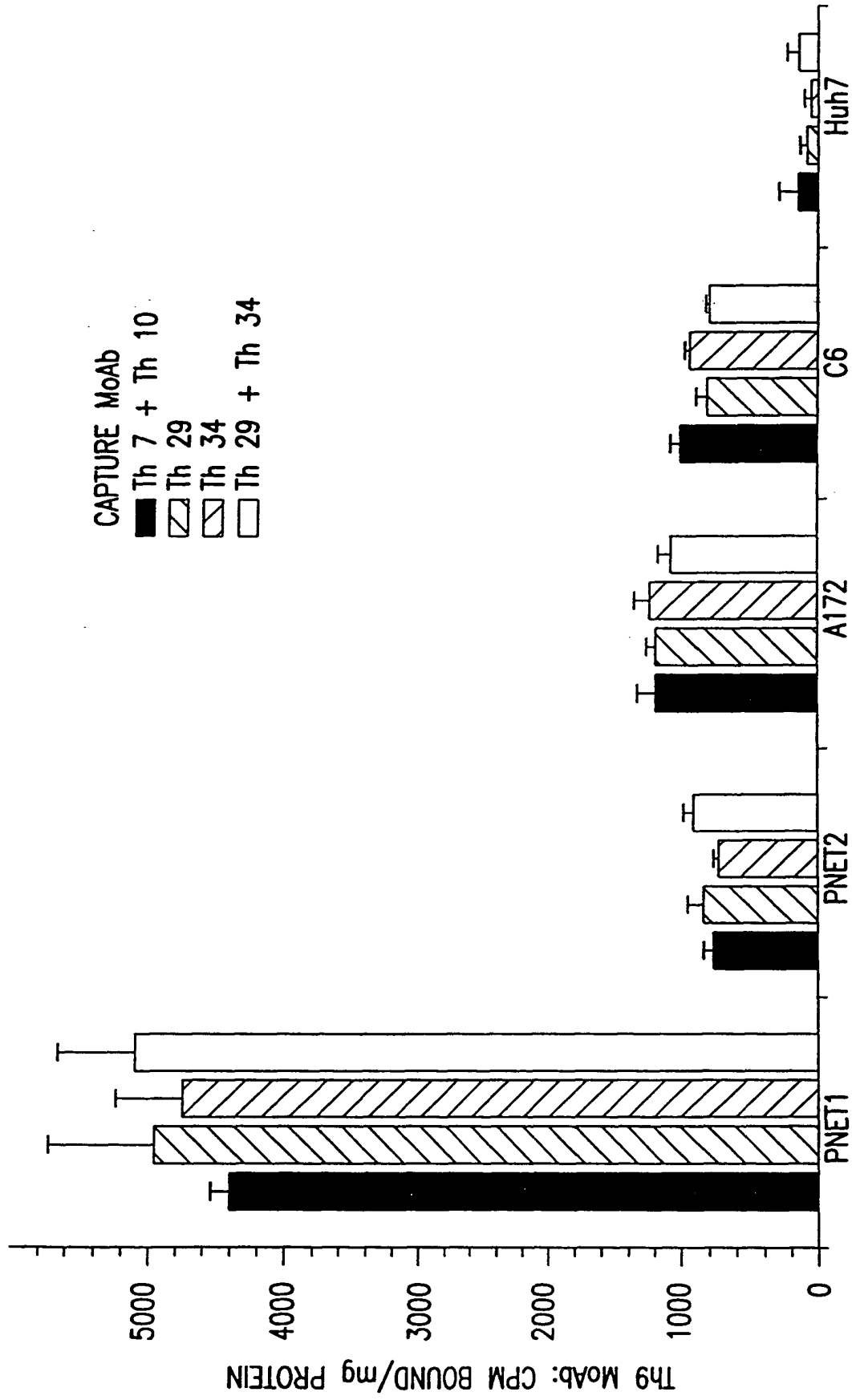


FIG.2

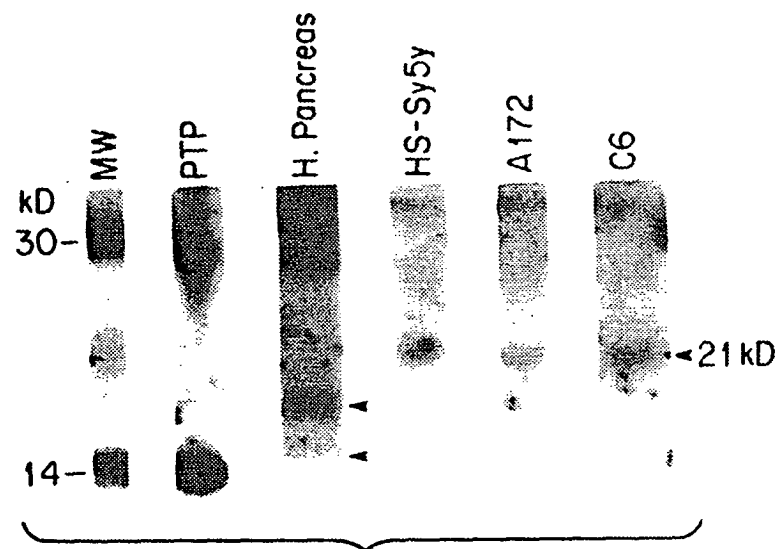


FIG. 3

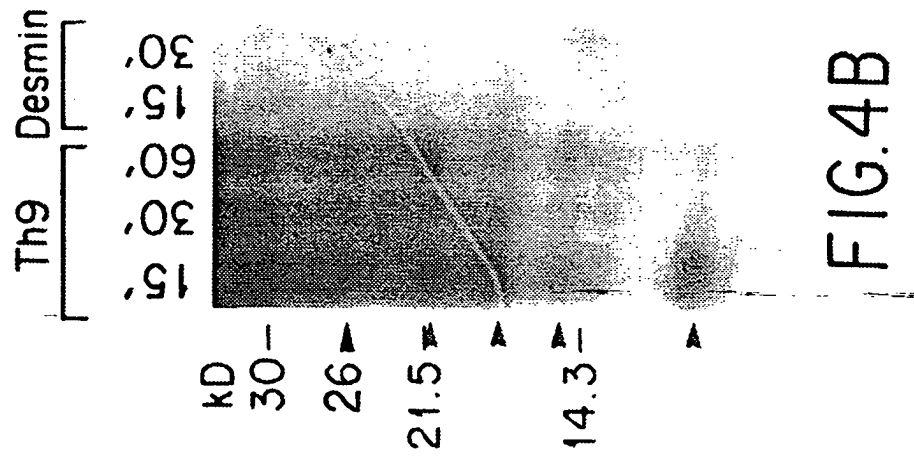


FIG.4B

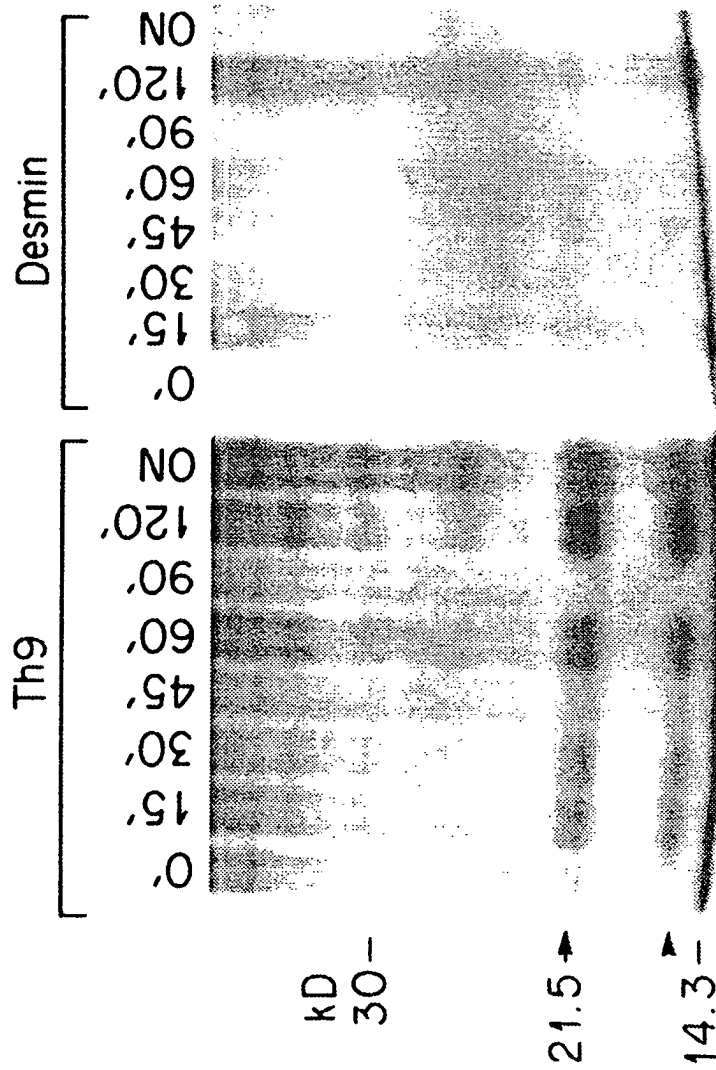


FIG.4A

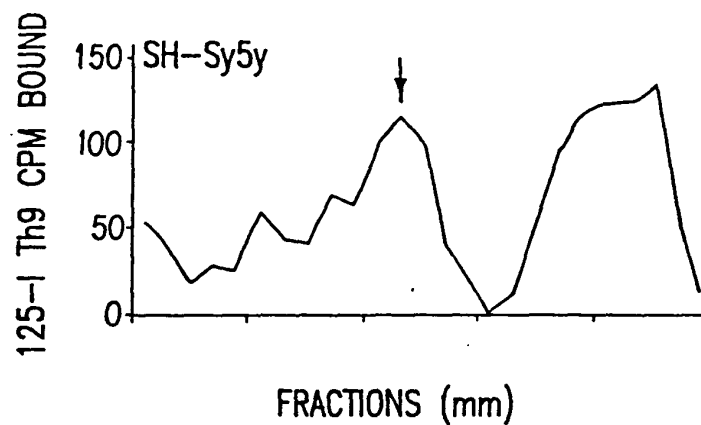


FIG. 5A

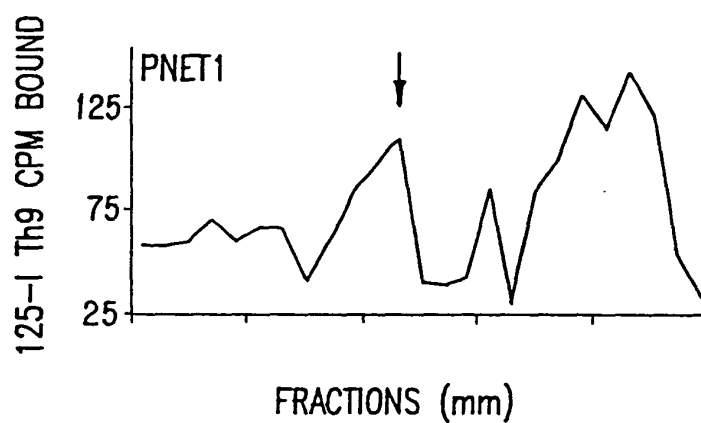


FIG. 5B

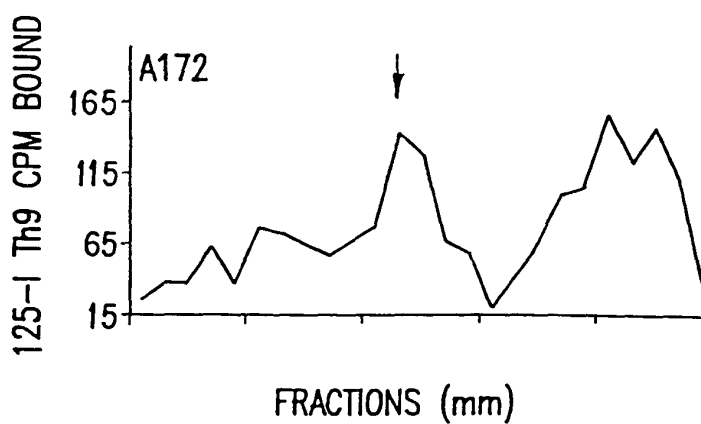


FIG. 5C

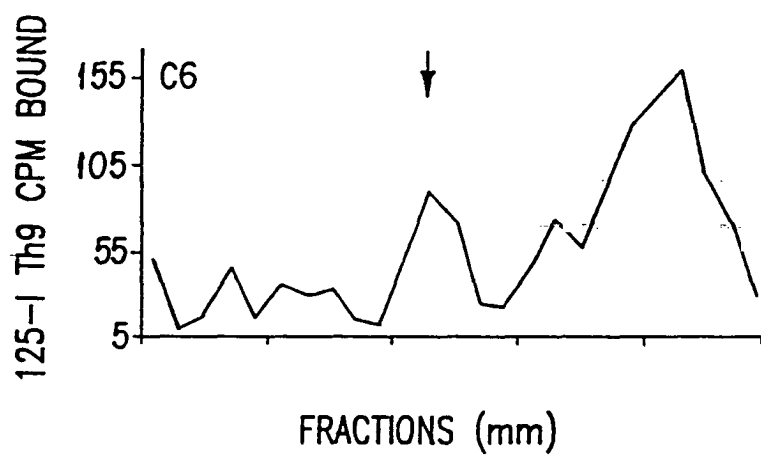


FIG.5D

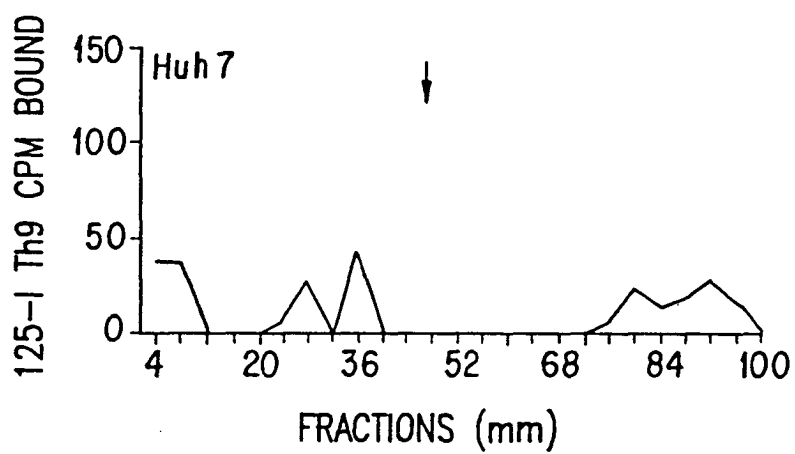


FIG.5E

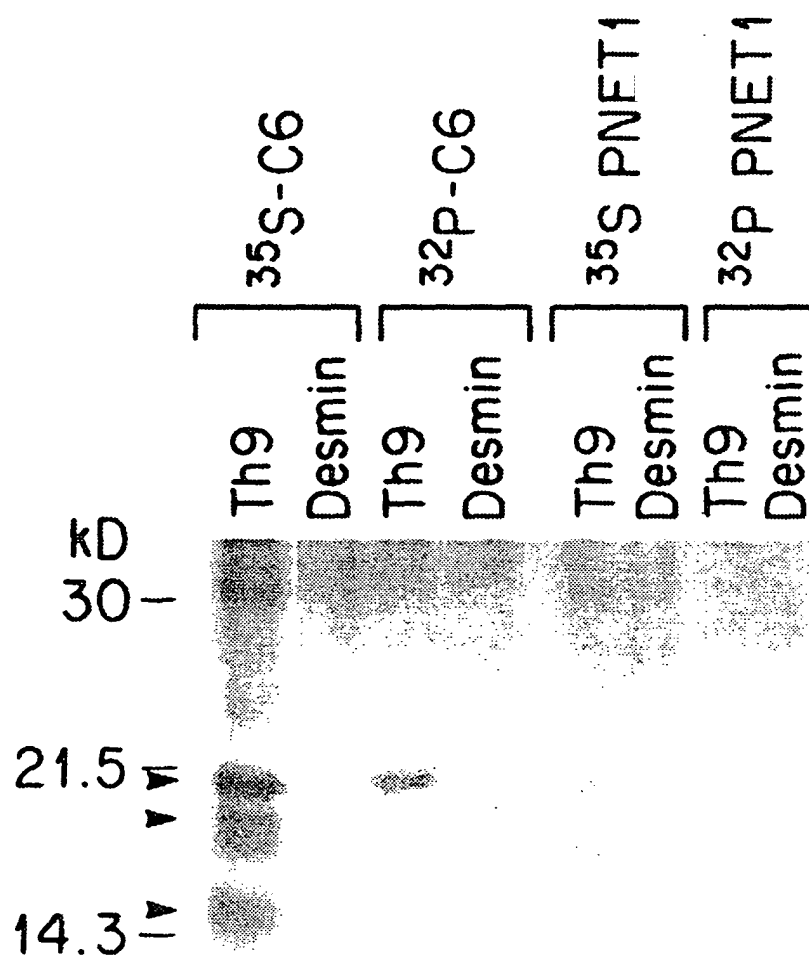


FIG. 6

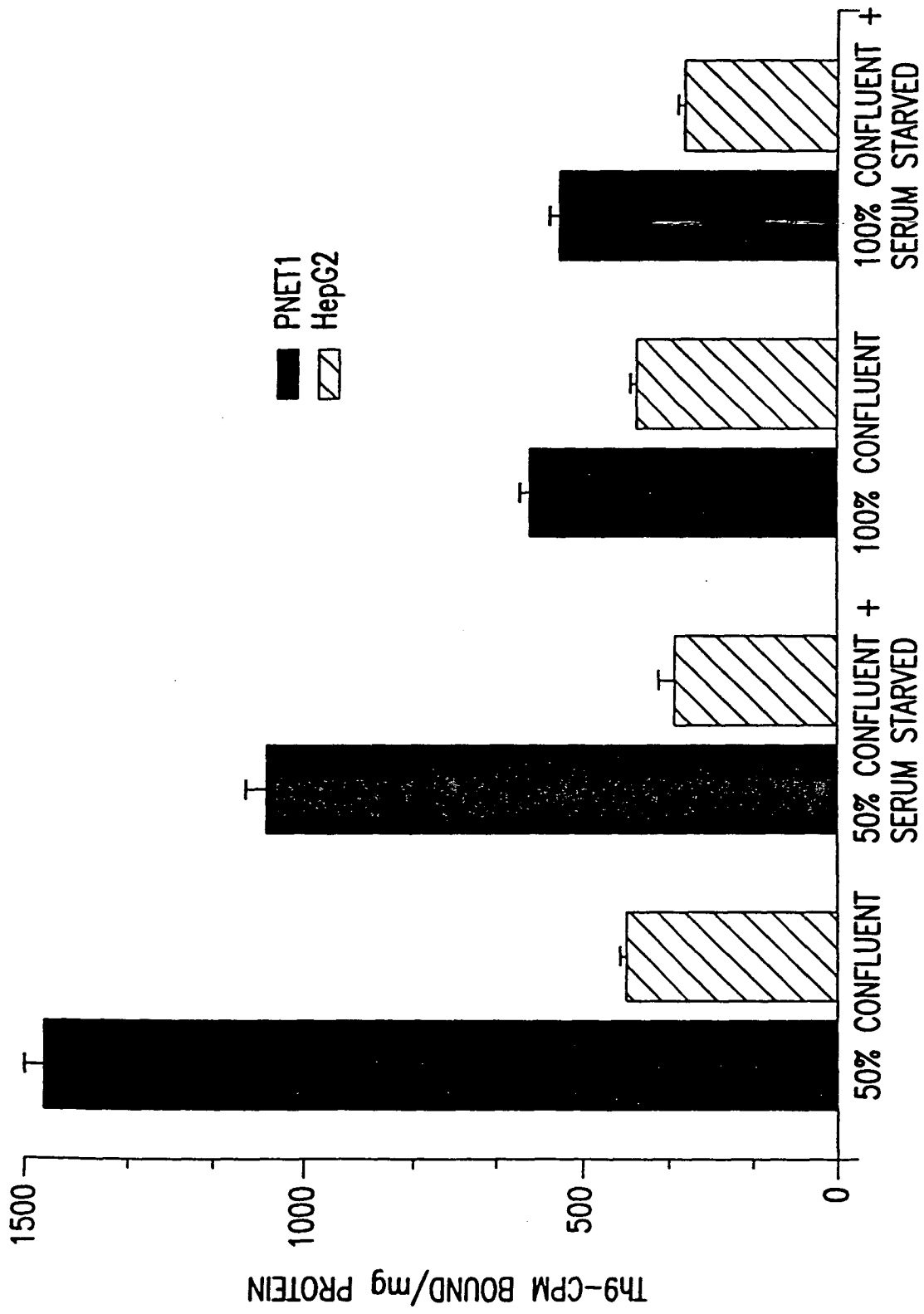


FIG.7



FIG. 8A

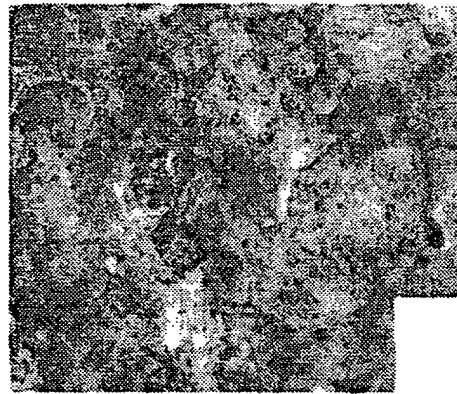


FIG. 8B

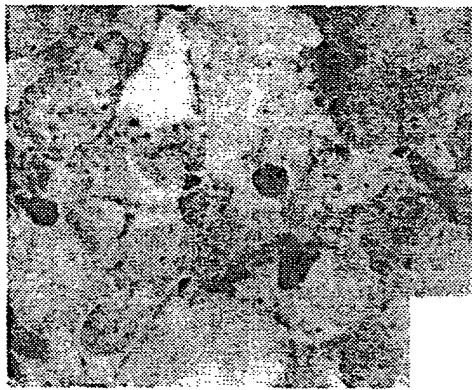


FIG. 8C

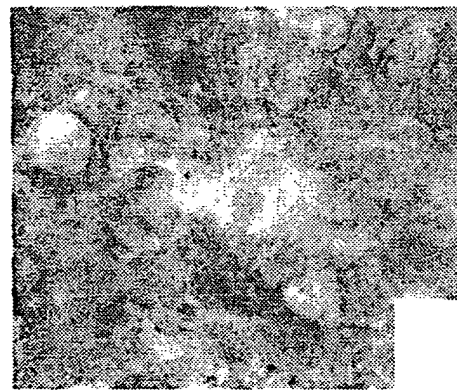


FIG. 8D

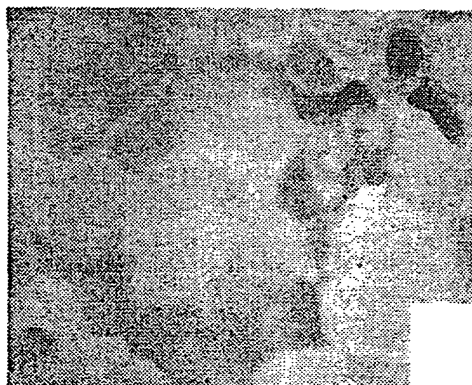


FIG. 8E



FIG. 8F

1-9a T7 SEQUENCE

Sequence Range: 1 to 1442

```

CGCTG CGCCC AGGCT GGCTC TGGAA AGCCT GTGCG GTCCT GGCAG GAAGC CCGGC CCGTG   60
GAGCA GGTTC TCGTT CTGCT TCAGC AATAA ATAAG GGTGA CCACA GGGAC TTTGC TTTTG  120
GTTTC CTTTC CTGTG AAAAG GTTGG TTTTA AAGTG AGATA CACTT TTCCG TAGAA CAAGT  180
GTTCT ATCTT TAAAA ACCCA AATTG CAGCA CCGTG GATTA CTGGT CTCAG AACAA CTCAT  240
TGCGC ATCAG ATTTG ACTCT CTGAT TTTCT GTCTA TTGGC CAAAT TGCCC TTTAA CTGCA  300
CCTGA ATCCT TTGTG TACTG ATGCC TTTGA CCTGG GCACC TTGGG AGAGT GTTGT GTTGC  360
TGTTT ACGGT TCTTC CTTCC CCTTG CTAAT TACAG TCTCT GGTGC CCAGC AAGCC CCTTT  420
GGCTT CCTTC CGTGA CTGGT CACGT TGTCT GCCTG GGCTC AGCGT GGACC TGCCC CATGC  480
TGCAG AACCT GGCCT CACCT GGACT TTTAC TAGAA TTGCC AGCTT CTCAA CTTAG CAGAT  540
CATCA CTCAT GCGGG CACAA GCAAA GATCA AACTT TTCTT TTTTG GTAAG CTTGA GTTTT  600
ACAAG TTATT TTTTG GTGAT GCGTA AGACA TTGCA GTGGG AAACC ATTCA ACTTG AGTTT  660
ATTGG AGTTT GCTGT TGTAG CAGGT TTTAA CTCAG GAACA ACTCT TGTCT GATCT CTCGC  720
CCCTC TGCCG GGACT ACATT ACTGT CTCTC GGAGC CCGTA GCGTT GCTGT CGAGT CCCAG  780
GACTA TCTCT GCAGA CTGCT ATGCT CAGAT CGAAG TATTT CACAA GAATA CTTGT GTTTT  840
TAACA GCCCT TCCCC TGGAC GGTGC GCCAT GAGGG CCTCA TGTTA GGCAT TGCCT TTTCT  900
TTCTG TGGAT CCAGT ATCTT CCTCG GCTTT TTAGG GAGCA GGAAA AATGC GTCTG AGAGC  960
AACTC TTTT AAAA CCTGC CCTGT TGTAT ATAAC TGTGT CTGTT TCACC GTGTG ACCTC 1020
CAAGG GGGTG GGAAC TTGAT ATAAA CGTTT AAAGG GGCCA CGATT TGCCC GAGGG TTAAT 1080
CCTTT GCTCT CACCT TGTAT GGATG AGGAG ATGAA GCCAT TTCTT ATCCT GTAGA TGTGA 1140
AGCAC TTTCA GTTTT CAGCG ATGTT GGAAT GTAGC ATCAG AAGCT CGTTC CTTCA CACTC 1200
AGTGG CGTCT GTGCT TGTCC ACATG CGCTG GCGGT CTGGA CCTTG AATGC CTGCC CTGGT 1260
TGTGT GGACT CCTTA ATGCC AATCA TTTCT TCACT TCTCT GGACA CCCAG GCGCG CTGTT 1320
GACAA GTGTG GAGAA ACTCC TAATT TAAAT GTCAC AGACA ATGTC CTAGT GTTGA CTAAT 1380
ACAAT GTTGA TGCTA CACTG TTGTA ATTAT TAAAC TGATT ATTTT TCTTA TGTCA AAAAA 1440
AAA

```

FIG.9

WP5' SEQUENCE

Sequence Range: 1 to 313

```

GATCC CGTTT GACAG GTGTA CCGCC CCAGT CAAAC TCCCC ACCTG GCACT GTCCC CGGAG
CGGTC GCGCC CGCGC GACCA CGGAG CTCTG GCGCG CAGAA GCGAG AGCCC CTCGC TGCCC
CCCGC CTCAC CCGGT AGTGA AAAAA CGATG AGAGT AGTGG TATTT CACCG GCGGC CCGCG
AGGAC CCCC GCGGA CCCAG TGCGG AACGG GGG

```

FIG.9A

9A+1-T7		5	10	15	20
[386]	_____	CACC	GtGg	TtA-C	tGtC>
Humon-PTP		CATT	GCAGC	TCAGC	ATGCC

9A+1-T7	25	30	35	40	45	50	55	60	65	70	75	
[386]	TCAGA	aCAaC	TCATt	gcgCA	T-CoG	ATtTo	CtctC	TGAIt	TTTCT	GTCTa	ttgGC	CAItG>
Human-PTP	TCAGA	CCAGC	TCATA	CTTCA	TGCTG	ATCTC	CTGCC	TGATG	TTTCT	GTCTC	AGAGC	CAAGG

9A+I-T7	85	90	95	100	105	110	115	125	130	135	140
[386]	CCcIt	LoaCt	gcacC	tGA-a	TcCIt	tgtGt	aClGA	TCcIt	TGagC	tG—G	GCACC -tTG->
Human-PTP	CCAAG	AGGCC	CAGAC	AGAGT	TGCCC	CAGGC	COGGA	TCAGC	TGCCC	AGAAG	GCACC AATGC

9A+I-T7 145 150 155 160 165 170 175 180 185 190 195
[386] ggAga G-T-g TtgTG tTgCT -gTT AcgGl tcttC cT-tc cCCTt GcTaa tTaCa G-TCT>
Human-PTP CTATC GCtCC TACTG CTACT ACtTT AATGA AGACC GTGAG ACCTG GGTtG ATGCA GATCT

9A+1-T7	200	205	210	215	220	225	230	235	240	245	250	255
[386]	CTggT	GCCAG	cA-Ag	ccccT	tTGCC	tTCCT	tccGT	gacTG	gTCAC	gttGt	CtGcc	tGgGC>
Human-PTP	CTATT	GCCAG	AACAT	GAATT	CGGGC	AACCT	GGTGT	CTGTG	CT Q C	CCAGG	CCGAG	GGTGC

9A+I-T7	260	270	275	280	285	290	300	305	310	315		
[386]	CagcG	TGCC	cCA-T	GcTgc	A-GAa	ccTGG	C-CTc	AgGAC	TTttc	acT-a	GaATT	GcCCT>
Human-PTP	CTTTG	TGCC	TCACT	GATTA	AGGAG	AGTGG	CACTG	ATGAC	TTCAA	TGTCT	GGATT	GGCCT

9A+I-T7	325	330	335	340	345	350	355	360	365	370	375	
[386]	tCcTc	A-aCl	tAgcA	GAtCa	tTCaC	Tcatg	CgGgC	aCA-a	Gcaa	gaTca	aCaCl	TtC-l>
Human-PTP	CCATG	ACCCC	AAAAA	GAACC	GCCGC	TGGCA	CTGGA	GCAGT	GGGTC	CCTGG	TCTCC	TACAA

9a-l7
[180]
H REG GENE

10 15 20 25 30 35 40 45

TT TTCCT AgA-A cA-aG -gGtT cTatC T-TTA A-AA -Accc aaATT>
TT CTCCT ATAGA GATTG TTGAT TTGCC TCTTA AGCAA GAGAT TCATT

9a-t7	50	55	65	70	75	80	85	90	95	100	105	110
[180]	GCAGC	aCcGc	tGtGc	TCAGa	aCAaC	TCATt	gcgCA	T-CaG	ATtTa	CTcLc	TGATt	TTTCT>
H REG GENE	GCAGC	TCAGC	ATGCC	TCAGa	CCAGC	TCATA	CTTCA	TGCTG	ATCTC	CTGCC	TGATG	TTTCT

9a-t7 115 120 125 130 135 140 145 150 155
[180] GTCTa tttGg CcAaa T-tGc cCT-T TTaaC tGcAc CtgAa TCITT>
H REG GENE GTCTC AGAGC CAAGG TAAGA TCTCT TTTCC ACCAA CCAAC TCITT

FIG. 10

9A+1-T7
[130]
EXON2

5 10 15 20 25 30
Cac cGtgG aTtA- CtGt CTCAG AaCAa>
CAT TGCAG CTCAG CATGG CTCAG ACCAG

9A+1-T7
[130]
EXON2

35 40 45 50 55 60 65 70 75 80
CTCAT tgcgC AT-Co GATtT aCTct CTGAT tTTTC TGTCT attgG CCAA>
CTCAT ACTTC ATGCT GATCT CCTGC CTGAT GTTTC TGTCT CAGAG CCAA

H REG GENE
[136]
WPO3-4 T7

5 10 15 20 25 30 35 40 45
G aATtc cTGgg cTCAa GtgAt CCTC- TCaLG caGTC TCC- CA-aA gT-GC>
G GAGTT TTGTC ATCAG GCCAG CCTCA TCCCG AGGTC TCCTC CACCA TTGGC

H REG GENE
[136]
WPO3-4 T7

50 55 60 65 70 75 80 85 95 100
tG-gG aTgaC AGGcT -tGaG C-CAC C-AcA -ccA ggCCC aT-Co TCAGt tTatA TAAAG>
CGTAG CCAGC AGGTT CAGTG CTCAC CGAAA GTAAA ATCCC CTCCT TCAGC AAGAA TAAAG

H REG GENE
[136]
WPO3-4 T7

105 110 115 120 125 130
aAAaA aAaAC CTTAa aaT-t gTtAg GcAA- ATA>
CAATA TACAC CTTAG GTTCC ACTAA GTAAC ATA

WPO3 8SP
[108]
EXON2

120 115 110 105 100 95 90 85 80 75
<GTT-c TgTGa gTCTc AAttt gttcc TTCTt gGaAG CT-G tCTGG -TgA- AtClG
GTTGA TTTGC CTCTT AAGCA AGAGA TTCAT TGCAG CTCAG CATGG CTCAG ACCAG

WPO3 8SP
[108]
EXON2

70 65 60 55 50 45 40 35 30
<tTggT cCcTC tgtCT GcToT tCTGt CTG-T cTgTo TGTCT -G-t CCAtG
CTCAT ACTTC ATGCT GATCT CCTGC CTGAT GTTTC TGTCT CAGAG CCAAG

FIG.10A

AD3-4-296 [112] WP5' 4/93	260 255 250 245 240 235 230	<ACTA CcaAa C-CT- -GCat tA-AA -aAa tttCg gTtG- -GtCg ACCA CCGAG CTCTG GGCGC CAGAA GCGAG AGCCC CTCGC TGCCC
AD3-4-296 [112] WP5' 4/93	225 220 215 210 205 200 195 190 185 180 175 170	<aCCtC -ggAg C-aGa AcccA Acctc CGAgc AGtac A-TGc TAaga CttCa cCaGt CaaaG CCCGC CTCAC CCGGT AGTGA AAAAA CGATG AGAGT AGTGG TATTI CACCG GCGGC CCGCG
AD3-4-296 [112] WP5' 4/93	165 160 155 150 145 140 135 130 125 120 115	<-cGA- aCgta ClatA ClCaA T-LG AtCca alaAc TtGoC CaacG Gaaca AgTTA ccCTA AGGAC CCCCg CCGGA CCCAG TGCGG AACGG GGGAG TAGTC CCGGG GGCTC ACTTA TTCTA
AD3-4-296 [112] WP5' 4/93	105 100 95 90 85 80 75 70 65 60 55 50	<tAacA G-CgC Aatcc tAttC TAGAG TcCaI aTCAA CAGGG TtToC gacCt CGoTG -TTgg CATTa GTCTC ACGTG CAGAC TAGAG TCAAG CTCAA CAGGG TCTTC TTTCC CGCTG ATTCC
AD3-4-296 [112] WP5' 4/93	45 40	<atCAg GoC GCCAA GTC
AD2 SP6F [504] 1-9AT7-3 3	10 15 20 25 30 35 40 45 50 55 60 65	AG-Tt TCaCT CTGtL gCCCA GGCTG gAGTG CAaTG GCaCA ATCct GGCTC ACTGC aAcCT> AGATC TCGCT CTGTC ACCCA GGCTG AAGTG CAGTG GCCCA ATCTC GGCTC ACTGC GAGCT
AD2 SP6F [504] 1-9AT7-3 3	70 75 80 85 90 95 100 105 110 115	CCgCC TCCCG aGcTC Aagca ATTCT CCTGC CTCA- -GCCT C-G- -TGA GccGC TGGGA> CCACC TCCCG GGTTC ACTTC ATTCT CCTGC CTCAC TGCCCT CAGCC TCTGA GTAGC TGGGA

FIG.10B

HB4-SEQ SEQUENCE

GAGGC GTATT ATACC ATGCT CCATC TGCCT ACGAC AAACA GACCT AAAAT CGCTC ATTGC	60
ATACT CTTCA ATCAG CCACA TAGCC CTCGT AGTAA CAGCC ATTCT CATCC AAACC CCCTG	120
AAGCT TCACC GCGGC AGTCA TTCTC ATAAT CGCCC ACGGG CTTAC ATCCT CATT A CTATT	180
CTGCC TAGCA AACTC AACTC ACGAA CGCAC TCACA GTGGC ATCAT AATCC TCTCT CAAGG	240
ACTTC AACTC CTACT CCCAC TAATA GCTTT TTGAT GACTT CTAGC AAGCC TCGCT AACCT	300
CGCCT TACCC CCCAC TATTA ACCTA CTGGG AGAAC TCTCT GTGCT AGTAA CCACG TTCTC	360
CTGAT CAAAT ATCAC TCTCC TACTT ACAGG ACTCA ACATA CTAGT CACAG CCCTA TACTC	420
CCTCT ACATA TTTAC CACAA CACAA TGGGG CTCAC TCACC CACCA CATT A ACAAC ATAAA	480
ACCCT CATT C ACACG AGAAA ACACC CTCAT GTTCA TACAC CTATC CCCCC TTCTC CTCCT	540
ATCCC TCAAC CCCGA CATCA TTACC GGGTT TTCCT CTTAA AAAAA AAAAA AAAA	590

HB4 PROTEIN

EAYYT MLHLP TTNRP KIAHC ILFNQ PHSPR SNSHS HPNPL KLHRR SHSHN RPRAY ILITI	60
LPSKL KLRTH SQSHH NPLSR TSNST PTNSF LMTSS KPR	95

FIG.11A

HB4 PROTEIN HYDROPHILICITY WINDOW PLOT

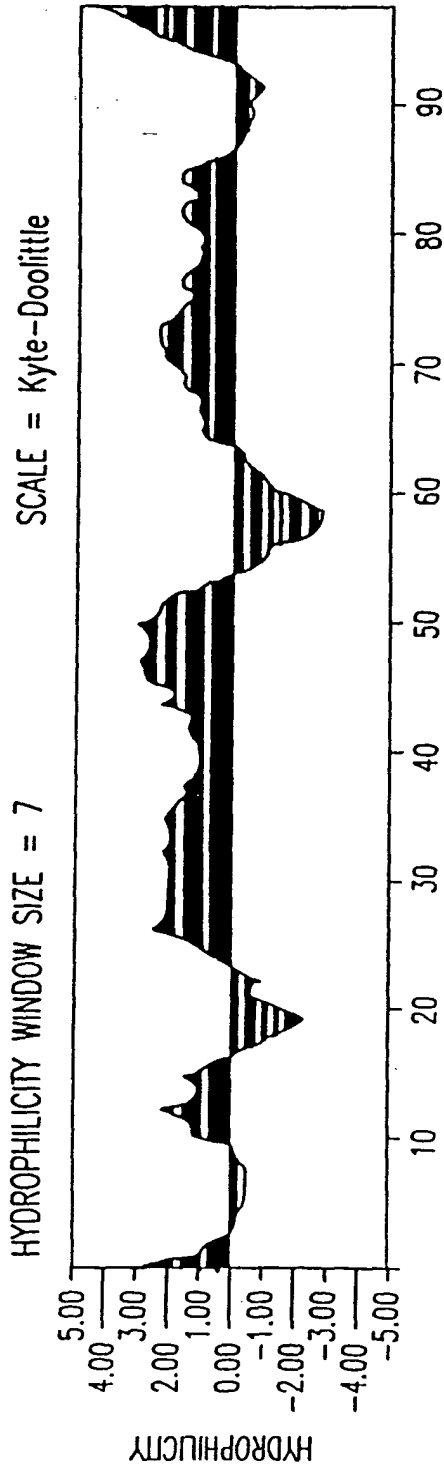


FIG.11B

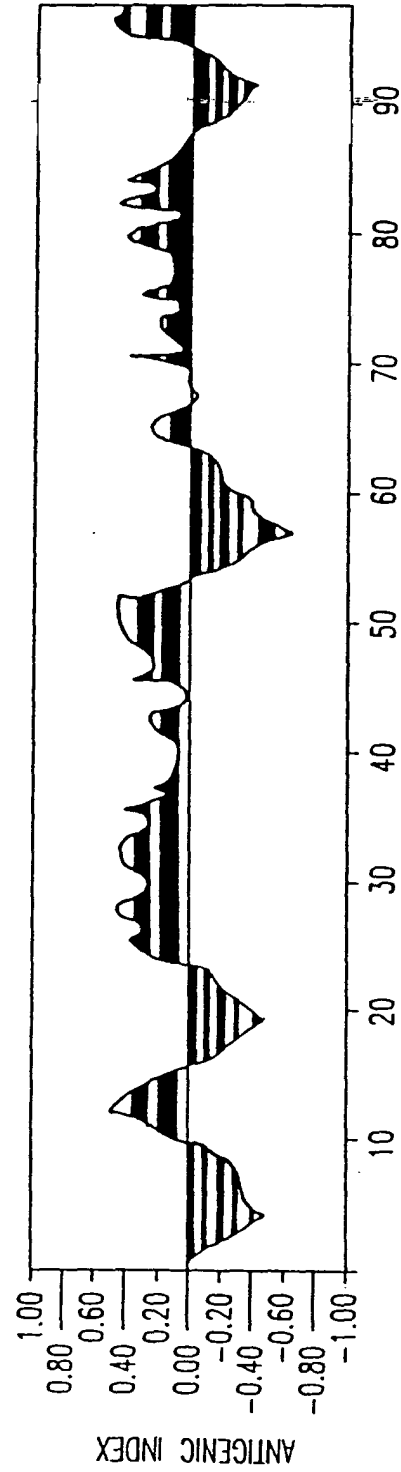


FIG.11C

HB4-SEQ
[440]
Human-PTP

ATaC>
ATGC

HB4-SEQ 15 20 25 30 35 40 45 50 55 60 65
[440] C-AT- GCTCC atCTG C-CT ACgac AA-ac AGACC -T-A- AaaTc GcTca tTGCA tA-CT>
Human-PTP CTATC GCTCC TACTG CTACT ACTTT AATGA AGACC GTGAG ACCTG GGTTG ATGCA GATCT

HB4-SEQ 70 75 80 85 90 95 100 105 110 115 120
[440] CTtca atCAG cACAT -Agcc CtcG- tAgta acaG- CcaTt CTCAt CCAaa CCccc tGaag>
Human-PTP CTATT GCCAG AACAT GAATT CGGGC AACCT GGTGT CTGTG CTCAC CCAGG CCGAG GGTGC

HB4-SEQ 125 130 135 140 145 150 155 160 165 170 175
[440] CTTca ccGgC gCAGt cATT- ctcAt AaTcG C-Cca cgGgC TTacA T-cCT -cATT actaT>
Human-PTP CTTTG TGGCC TCACT GATTA AGGAG AGTGG CACTG ATGAC TTCAA TGTCT GGATT GGCCT

HB4-SEQ 180 185 190 195 200 205 210 215 220 225 230 235
[440] tC-TG cCaqC AAAct cAAaC taCGa acCCA CT-ca -CAGT cGcat CaTaa TCTCt ctCAA>
Human-PTP CCATG ACCCC AAAAA GAACC GCCGC TGGCA CTGGA GCAGT GGGTC CCTGG TCTCC TACAA

HB4-SEQ 240 245 250 255 265 270 275 280 285 290 295 300 305
[440] GgaCT -tcaa AcTct ActCC CAAGC tTGT gAcTt CTaGC aACct cGctA aCCTc gCCTt>
Human-PTP GTCCT GGGGC ATTGG AGCCC CAAGC AGTGT TAATC CTGGC TACTG TGTGA GCCTG ACCTC

HB4-SEQ 310 315 320 325 330 340 345 350 355 360 365 370
[440] AccCc CActA TTaac ctAcT GGgAG aATGT G-CTa GT-AA -cCAc GTTCT CCTTc aaaTa>
Human-PTP AAGCA CAGGA TTCCA GAAAT GGAAG GATGT GCCTT GTGAA GACAA GTTCT ccTTT GTCTG

HB4-SEQ 375 380 385 390 395 400 405 410 415 420 425
[440] tcAcT ctccT ActTA cAGG- A-CT- cAAcA TACta GTCcA GccCT -ATaC tcCct cTACA>
Human-PTP CAAGT TCAAA AACTA GAGGC AGCTG GAAAA TACAT GTCTA GAACT GATCC AGCAA TTACA

HB4-SEQ 430 435 440 445 450 455 460 465 470 475 480 485
[440] ttttt acCAc AAcac AAtgg GGctC A-CTC aCCcA C-CAc aTtAA CCata AaACc CTCaT>
Human-PTP ACGGA GTCAA AAATT AAACC GGACC ATCTC TCCAA CTCAA CTCAA CCTGG ACACT CTCTT

HB4-SEQ 490 495 500 505 510 515 520 525 530 540 545
[440] -TCac acGAG -aaaa Ccccc TcAtg TTC-A TAcac cTA- TcCCC CAITC TTcct AtCCc>
Human-PTP CTCTG CTGAG TTTGC CTTGT TAATC TTCAA TAGTT TTACC TACCC CAGTC TTTGG AACCT

HB4-SEQ 550 555 560 565 570 575 580 585 590
[440] TcAAc cccgA cAtcA AcCgg GTTTC CtCTt AAAAA AAAAA AAAAA A>
Human-PTP TAAAT AATAA AAATA AACAT GTTTC CACTA AAAAA AAAAA AAAAA A

FIG.11D

H REG GENE 2260 2265 2270 2275 2280 2285 2290 2295 2300 2305
 [284] —C tTcTT -TtTC AgGC- CoAgo gGCCc A-GAC AgAgt tgCC- ccAgg CcCgg ATcag>
 HB4-SEQ C GTATT ATACC ATGCT CCATC TGCCT ACGAC AAACA GACCT AAAAT CGCTC ATTGC

H REG GEN2310 2315 2320 2322330 2335 2340 2345 2350 2355 2360 2365 2370
 [284] cTgCc CagaA ggCAc CaACc TAlCg CTCcT AcT-g ClcCl AcTtT aATga AgACC gCgaG>
 HB4-SEQ ATACT CTTCA ATCAG CCACA TAGCC CTCGT AGTAA CAGCC ATTCT CATCC AAACC CCCTG

H REG GBNE 2375 2380 23852390 2395 2400 2405 2410 2415 2420 2425 2430
 [284] -AcCTt gggtt GatGC AGTgt gagTg AggAg aCCgt glGGG aaggg AgaCT CATga -aggg>
 HB4-SEQ AAGCT T QCC GGCGC AGTCA TTCTC ATAAT CGCCC ACGGG CTIAC ATCCT CATTA CTATT

H REG GENE 2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485
 [284] agGgg aAGC- tgC-C ActCT -CcAg tGtgt TCAgt GgCGC Aatga gAT-g agaCT gAAcc>
 HB4-SEQ CTGCC TAGCA AACTC AAAC TACGA ACGAC TCACA GTCCG ATCAT AATCC TCTCT CAAGG

H REG GENE 24902495 2500 2505 2510 2515 2520 2525 2530 2535 2540
 [284] cCTTt AIACT aTcaT CagcC ccA-A aCTTT ccoAT -CTa CT-l tAlCC -CatT AltCa>
 HB4-SEQ ACTTC AAAC TACTC CCCAC TAATA GCTTT TTGAT GACTT CTAGC AAGCC TCGCT AACCT

H REG GENE2545 2550 2555 2560 2565 2570 2580 2585 2590 2595 2600
 [284] gcaCa TlCCC agCAC aAagA ACCTg gTGGG tG-AC agcaT catC- AcggA Catta cTCTg>
 HB4-SEQ CGCCT TACCC CCCAC TATTA ACCTA CTGGG AGAAC TCTCT GTGCT AGTAA CCACG TTCTC

H REG GEN2605 2610 2612620 2625 2630 2635 2640 2645 2650 2655 2665 2670
 [284] CTG-T CcttT tTCAC cCTCC T-CTT ggAGG ACTCA gLATA tccGT CACAa CCCTc cACTg>
 HB4-SEQ CTGAT CAAAT ATCAC TCTCC TACTT ACAGG ACTCA ACATA CTAGT CACAG CCCTA TACTC

H REG GENE 2675 2680 2685 2690 2695 2700 2705 2710 2715 2720
 [284] agTCT cCAT- TTT-C tTC- tgCAA ca-G CTCta T-tgC CAgaA CATga A-ttC gggcA>
 HB4-SEQ CCTCT ACATA TTTAC CACAA CACAA TGGGG CTCAC TCACC CACCA CATT ACAA ACATA

H REG GENE 2725 2730 2735 2740
 [284] A-CCT -ggTg tC-tG tG-c tCACC C>
 HB4-SEQ ACCCT CATTC ACACG AGAAA ACACC C

FIG.11E

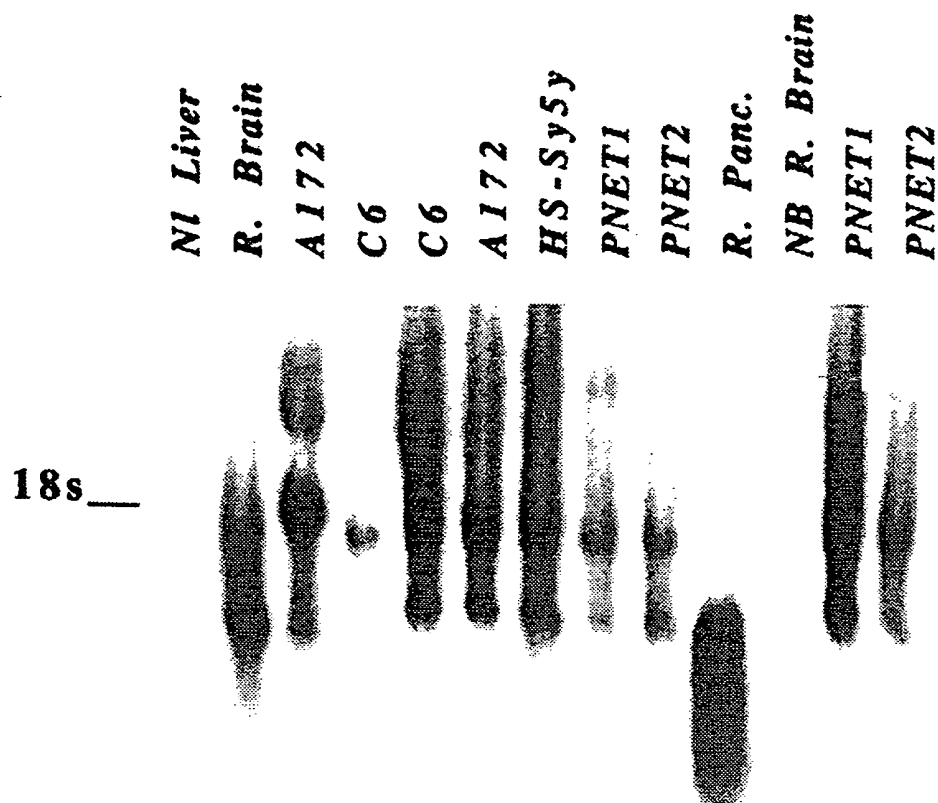


FIG.12A

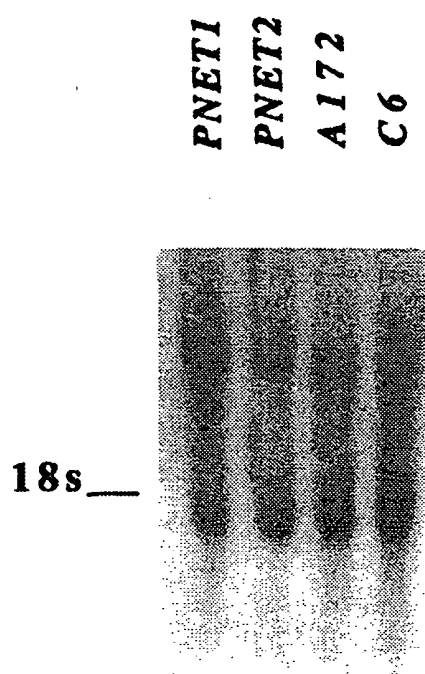


FIG.12B

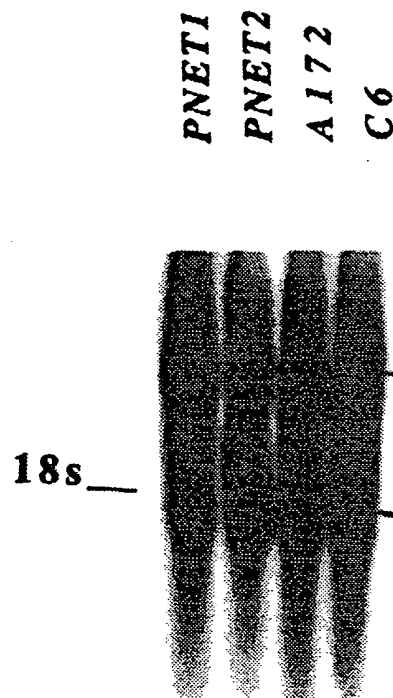


FIG.12C

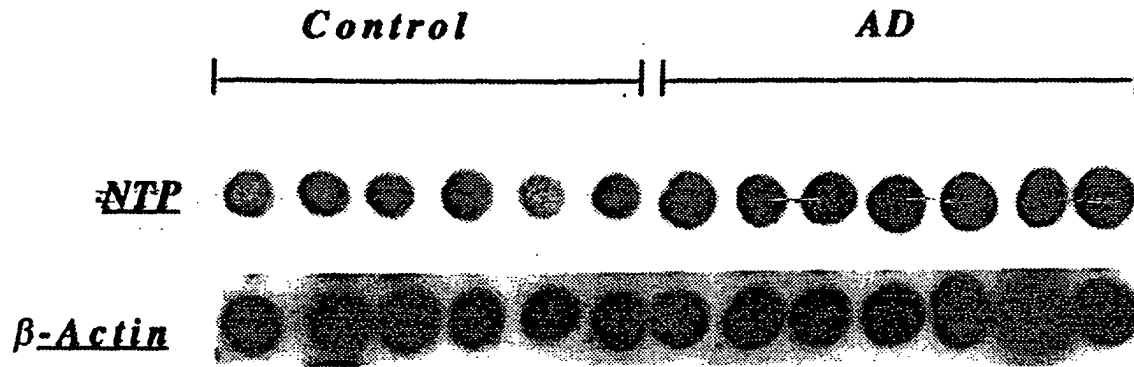


FIG. 13A

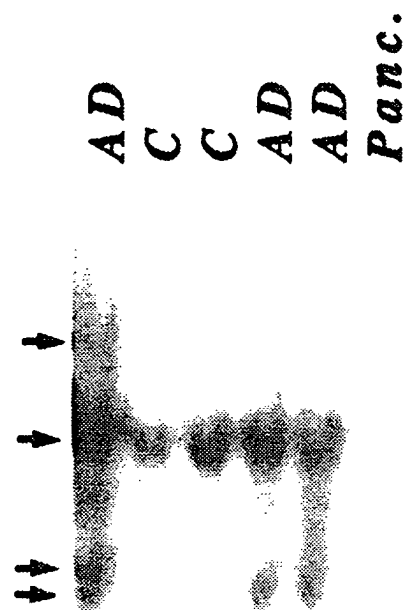
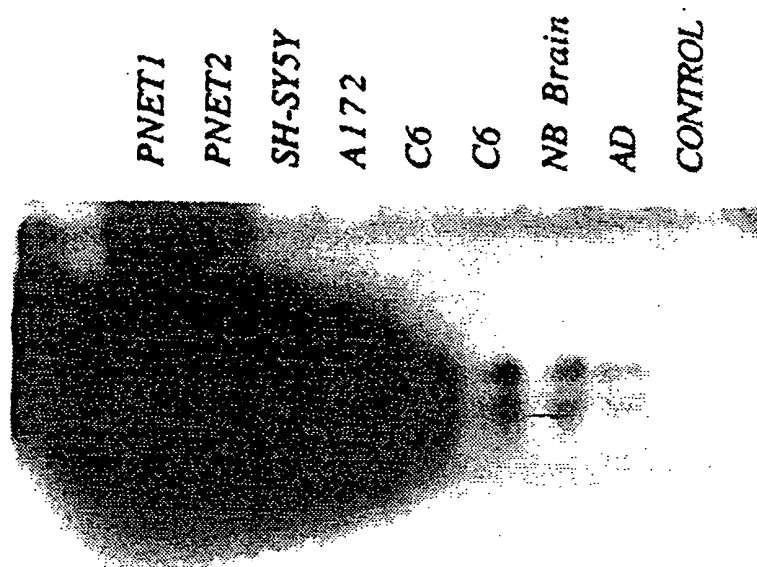


FIG. 13B



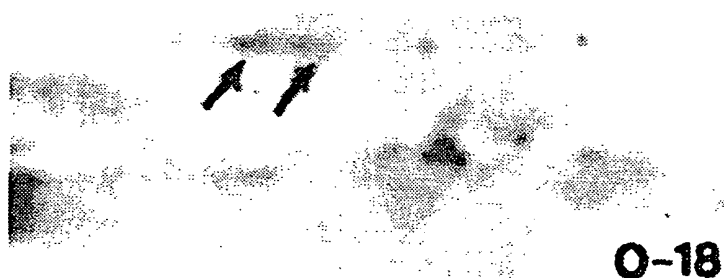
1-9a

FIG.14A



1-9a

FIG.14B



O-18

FIG.14C

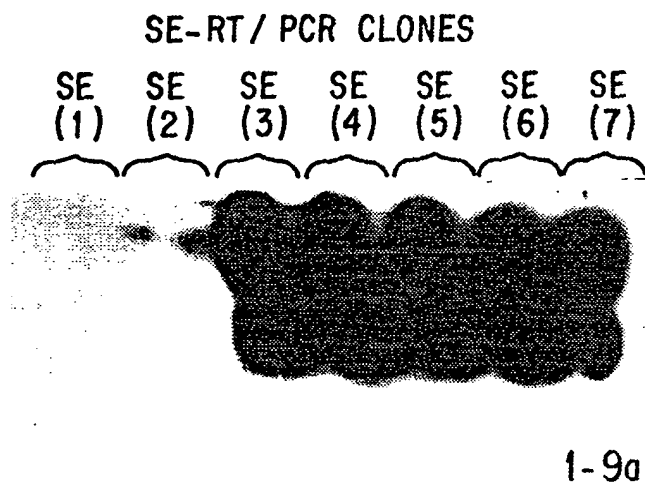


FIG. 15A

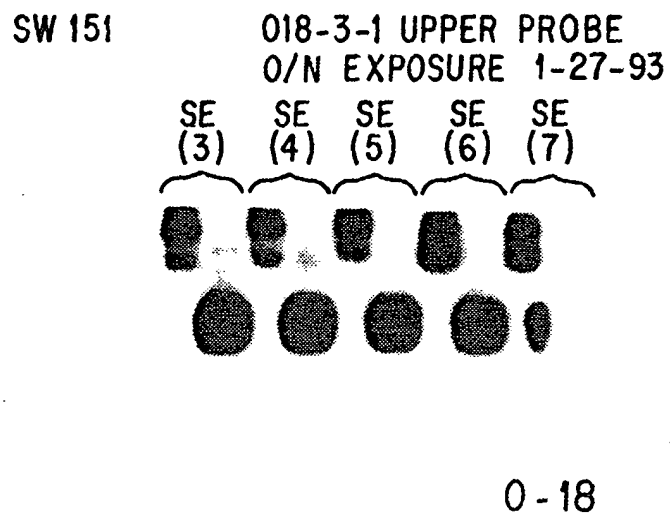


FIG. 15B

AD2-2 T7

```

GTTCT TAGTC TATCT CTTGT ACAAA CGATG TGCTT TGAAG ATGTT AGTGT ATAAC AATTG   60
ATGTT TGTTC TCTGT TTGAT TTAA ACAGA GAAAA AATAA AAGGG GTTAA TAGCT CCTTT  120
TTTCT TCTTT CTTT TTTT TTCAT TTCAA AATTG CTGCC AGTGT TTTCA ATGTA GGACA  180
ACAGA GGGAT ATGCT GTAGA GTGTT TTTAT TGCCT AGTTG ACAA GCTGC TTTG AATGC  240
TGGTG GTTCT ATTCC TTTGC ACATC ACGAC ATTTT ATAAT CATAG TTAAT TCGTA TATGA  300
CAAAA ATGCT CTGAT CTGAT GCCAA AGGTC AATTC AGTGT ATATA ACCTG AACAC ACTCA  360
TCCAT TCGCT TT                                     372

```

AD2-2 T7 PEP

```

MFVFC LILNR EKIKG GNSSE FLLSF FFSFQ NCCQC FQCRT TEGYA VECFY CLVDK AAFEC   60
WWFYS FDT

```

FIG.16A

AD2 SP6F

```

ACTGT CTCCC CCTTT GATAG GGACA CTAAA GTGGT CTGTA CTTGG GTAGA GGATG GCANG   60
TTAAG AATTA AAATC GTCTG GGTGC GGTCT GCAAG CTTGT AATCC CAGCA CTTG GGAGG  120
CTGAG GCGGG CGGAT CACCT GAGGT CAGGA GTTCG ACACC AGCCT GATGA ACATG GAGAA  180
ACCCC ATCTC TACTA AAAAT ACAA TATTA GCTGG GCGTT GTCCG GCGCC TGTA TCCA  240
GCGGC TCACG AGGCT GAGGC AGGAG AATTG CTTGA GCTCG GGATG GCGGA GGTG CAGTG  300
AGCCA GGATT GTGCC ATTGC ACTCC AGCCT GGGCA ACAAG AGTGA AACTC TGTCT CAAAA  360
AAAAA AAAAA AAAAA AA                                     377

```

FIG.16D

AD2-2 T7 HYDROPHILICITY WINDOW PLOT

HYDROPHILICITY WINDOW SIZE = 7 SCALE = Kyte-Doolittle

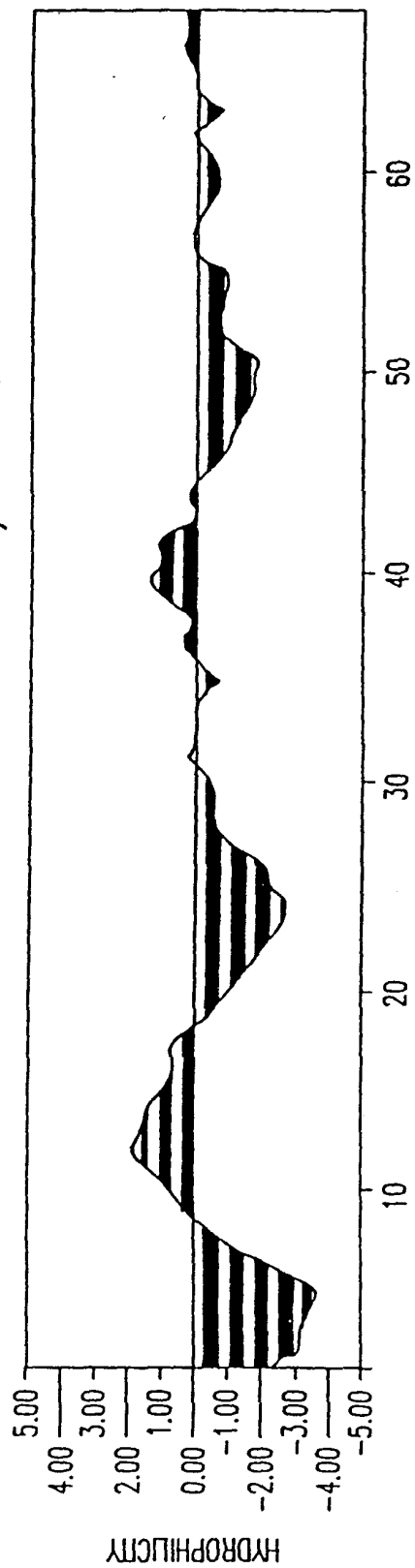


FIG.16B

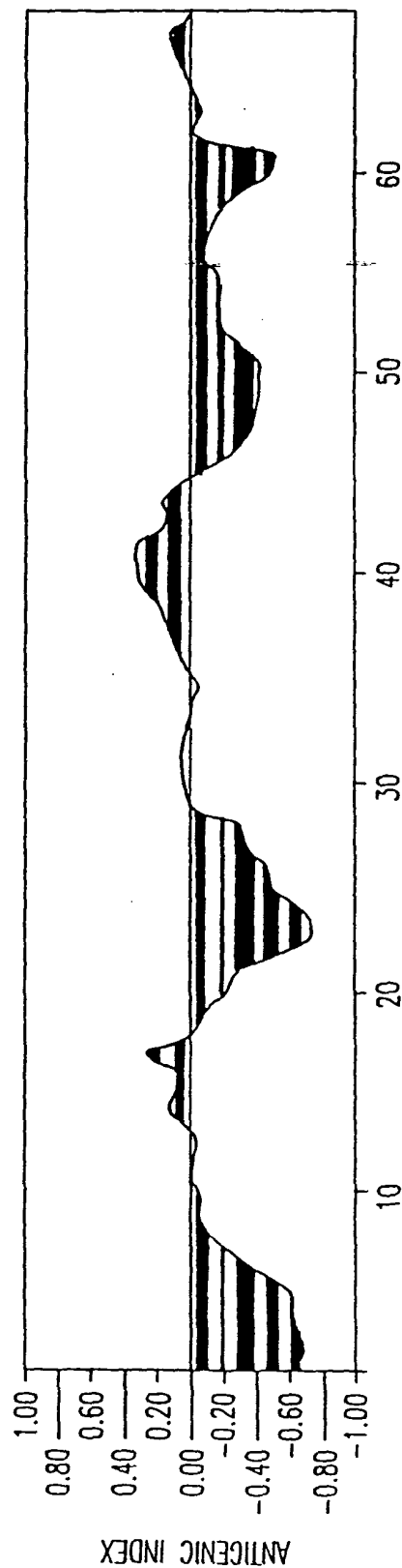


FIG.16C

AD2-2 SEQUENCE

```

GCGTAAACAC ATTTTGTTC TTAGTCTATC TCTGTACAA ACGATGTGCT TTGAAGATGT 60
TAGTGTATAA CAATTGATGT TTGTTTCTG TTTGATTTTA AACAGAGAAA AAATAAAAGG 120
GGGTAATAGC TCCTTTTTTC TTCTTTCTTT GATTTTAAAC AGAGAAAAAA TAAAGGGGG 180
TAATAGCTCC TTTTTCTTC TTTCTTTTTT TTTTTCATT TCAAAATTGC TGCCAGTGTT 240
TTCAATGATG GACAACAGAG GGATATGCTG TAGAGTGTTT TATTGCCTAG TTGACAAAGC 300
TGCTTTGAAT GCTGGTGGTT CTATTCCTTT GACACTACGC ACTTTTATAA TACATGTAA 360
TGCTATAGGA CAAGATGCTC TGATTCCTGA GTGCCAGAGG TTCAATTCAG TGTATATAAC 420
TGAAACACACI CATCCATTG TGCTTTTGT TTTTATGG TGGCTTAAAG GTAAAGAGCC 480
CATCCTTIGC AAGTCATCCA TGTGTACT TAGGCATTTT ATCTTGGCTC AAATTGTTGG 540
AAGAATGGTG GCTTGTTC TGGTTTTGT ATTTGTGTCT AATGCACGTT TTAACATGAT 600
AGACGCAATG CATTGTGTAG CTAGTTTTCT GGAAAAGTCA ACTCTTTTAG GAATTGTTTT 660
TCAGATCTTC AATAAATTTT TTCTTTAAAT TTCAAAGAAC AATGTGCTTG TGTGATGCC 720
TTACAAAAAC CATTGTATAT TTGTGATTC CTCTGTAT TTAGACAGTG GTTTTTCAGG 780
TGGGTGCTTT GTTTCTGGT ATGGCCTTTA TGAATGAGA CGCTTTAGCT TTGGTACGTA 840
GCGTAATCC ATAGCAGCTT TGGCAGTTT GTGTCTGAG TCTAGCTAA AAAGTTAGAA 900
GTTTACATGA CTGTTTTTTT TATTTCCCT AAATTATTAC TTAGCTGAG CATTAATTAA 960
GGGCATTTTC ACCTGTGTAA AATTATGGTC AGCTTTTTTC TGTCTATAAT TGTTTACTTT 1020
TGTGGGTTTA CTCTAGAAAC ATGAGCCAAA AATGTCAATA GACAACACAG TATTAATAA 1080
ACCCAAAAGT TGTAAGGGC AACGTTTCTC CCCTTTGATA GGGACACTAA AGTGGTCTGT 1140
ACTTGGGTAG AGGATGGCAG ACGTTAAGAA TAAAATGCC TCTGGGTGCC GTCTCACGCT 1200
TGTAATCCCA GCACTTTGGG AGGCTGAGGC GGGCGGATCA CCTGAGGTCA GGAGTTGAC 1260
ACCAGCCTGA TGAACATGGA GAAACCCCAT CTCTACTAAA AATACAAATA TTAGCTGGGC 1320
GTTGTCCGC GCCTGTAATC CCAGCGGCTC ACGAGGCTGA GGCAGGAGAA TTGCTTGAGC 1380
TCGGGATGGC GGAGGTGCA GTGAGCCAGG ATTGTCCAT TGCCTCCAG CCTGGGCAAC 1440
AAGAGTGAAG CTCTGTCTCA AAAAAAAAAA AAAAAAAAAA 1480

```

FIG.16E

AD3-4 SEQUENCE

ttgggtgaggtggo
 ATGAT GGTCT GTTGG AATCG GTTTG GTAAA TGGGT TTATT TCATA TCCGC TATCT TTAAC 60
 TTGG ACCGC GTTAT CTATA TCATG GCGTT CCTTT CTACT TTTA ATATT GGTTC GTATT 120
 ATATC GTTCC TGATT GGGGA TATGG AAGAC GTATT ACTTA ATTGT ACTTT ATTGA AACGT 180
 TCCTC TCGGT TTCGA TTCTG GGGGC TTTGG TCTGC TCGAT GGATT CTTGT CGATT TTCTC 240
 GTGTG GCAGT AACAT ACCGT TTTAT CACCC TTCTA AATAT CCCAT CTCCC GCTGT TTGGT 300
 AGGCT CGGAA CACTA TCGAC CAACA GGTTC TATCT AGAAT CAAGT TGGAA ATTAA ACGGT 360
 GTCTT GG 367

AD3-4 PROTEIN

MMVCW NREGK WYFI SAIFN FGPRY LYHGV PFYFL ILVRI ISFLI GDMED VLLNC TLLKR 60
 SSRFR FWGAL VCSMD SCRFS RVAVT YRFIT LLNIP SPAW MARNT IDQQV LSRIK LEIKR 120
 CL 122

FIG.16F

AD3-4T7

CCCAC AGGTC CTAAA CTACC AAACC TGCAT TAAAA AATTT CCGTT GGTCC ACCTC GGAGC 1180
 AGAAC CCAAC CTCCG AGCAG TACAT GCTAA GACTT CACCA GTCAA AGCGA ACGTA CTATA 1240
 CTCAA TTGAT CCAAT AACTT GACCA ACGGA ACAAG TTACC CTAGG GATAA CAGCG CAATC 1300
 CTATT CTAGA GTCCA TATCA ACAAT AGGGT TTACG ACCTC GATGT TGGAT CAGGA CATCC 1360
 CGATG GTGCA GCCGC TATTA AAGGT TCGTT TGTTT AAACG ATTAA AGTCC TCGTG TCTGA 1420
 GTTCA GACCG AAGTA ATCCA GGTCC GTTTC TATCT TCTTC AAATT CCTCC CTGTA CCGAA 1480
 AGGAC TAATG AGAAA TAAGG CCTAC TTCAC AAAGC GGCCT TCCCC CGTAA TGATA TCATC 1540
 TCAAC TTAGT ATTAT ACCCA CACCC ACCCA AGAAC AGGGT TTGTT AAAAA AAAAA AAAAA 1600

FIG.16I

AD3-4 HYDROPHILICITY WINDOW PLOT

HYDROPHILICITY WINDOW SIZE = 7 SCALE = Kyte-Doolittle

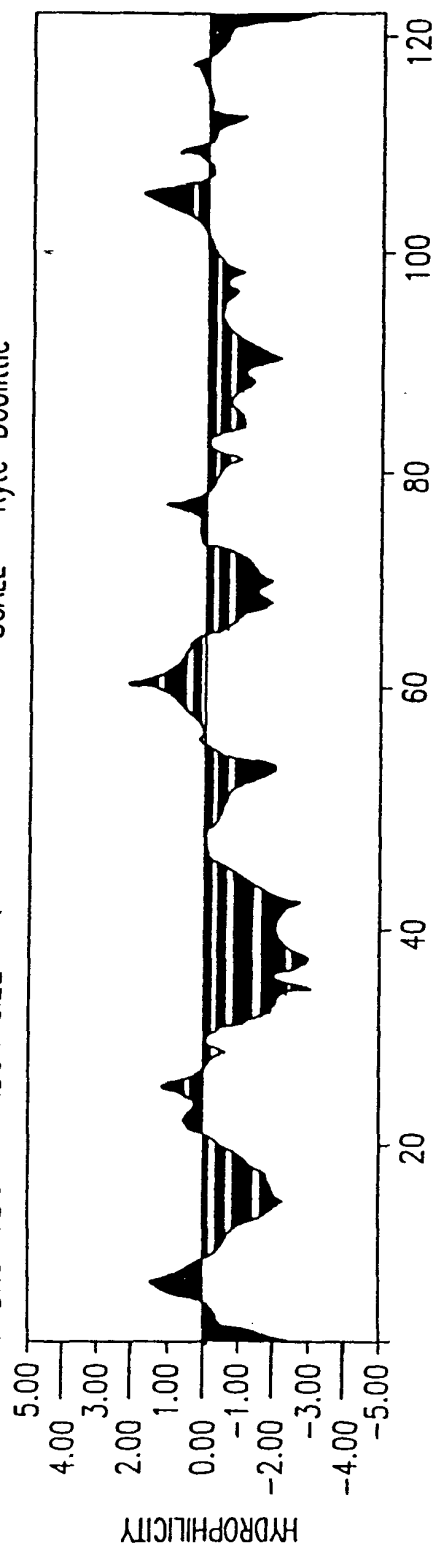


FIG.16G

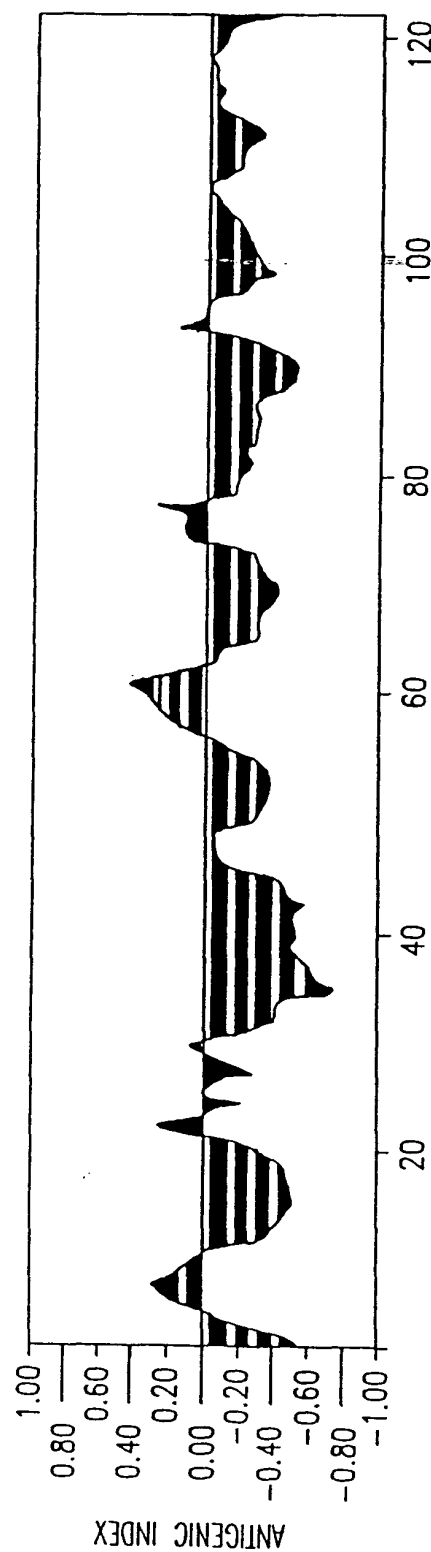


FIG.16H

AD3-4SP SEQUENCE

```

AACCCACTCC ACCTTACTAC CAGACAACCT TAGCCAAACC ATTTACCCAA ATAAAGTATA 60
GGCGATAGAA ATTGAAACCT GGCGCAATAG ATATAGTACC GCAAGGAAAG ATGAAAAAAT 120
ATAACCAAGC ATAATATAGC AAGGACTAAC CCCTATACCT TCTGCATAAT GAATTAACAT 180
GAAATAACTT TGCAAGGAGA GCCAAAGCTA AGACCCCGA AACCAGACGA GCTACCTAAG 240
AACAGCTAAA AGAGCACACC GTCATTGTAT GGCAAAATAG TGGGAAGATT TATAGGCTAG 300
AGGGCGACAA ACCATCCGAG CCTTGTGATA GCTGGTTGTC CAAGATAGAT CTTAGTTCAA 360
CCTTTAATTT GCCACAGAAC C 381

```

FIG.16J

AD3-4T7 SEQUENCE

```

TTTTTTTTTT TTTTAAACAA ACCCTGTTCT TGGGTGGGTG TGGGTATAAT ACTAAGTTGA 60
GATGATATCA TTACGGGGGA AGGCCGCTTT GTGAAGTAGG CCTTATTCT CATTAGTCCT 120
TTCGGTACAG GGAGGAATTT GAAGAAGATA GAAACCGACC TGGATTACTT CCGTCTGAAC 180
TCAGACACGA GGACTTTAAT CGTTTGAACA AACGAACCTT TAATAGCGGC TGCACCATCG 240
GGATGTCCTG ATCCAACATC GAGGTGTAAC ACCCTATTGT TGATATGGAC TCTAGAATAG 300
GATTGCGCTG TTATCCCTAG GGTAACCTGT TCCGTGGTC AAGTTATTGG ATCAATTGAG 360
TTTAGTAGTC CGCTTGGAGT GGTGAAGTCT AGAATGTCCT GTTCGGGGGT TGGTTTCTGC 420
TCCAGGTGCG CCCCAACCGA ATTTTTTATT GAAGGTGGG TAGTTTAGCA CCTGTGGGTT 480
GGTAAGGTAC TGTTGAATT AATAAATTA AGCTCCATAG GGTCTCCTCG TCTTGTGTC 540
TAATGCCCCC CTCTCCACGG GAAGTCAAT TCCACTGGT AAAAGTAAGA GAAAGCTGAA 600
CCCTCGGGGA GCCATCCATA CAGGTCCCC 629

```

FIG.16K

AD4-4 SP6 SEQUENCE

Sequence Range: 1 to 256

```

GCGGG TAAAT TGGTT TGTTA TTTTT TAAAA AAAAC TTGCA TGTTT AAAAA AAAGT TGATT 60
GCTTC AAATT TCTGC TACTA ACTTC AAGCT ATGGG AGTTT GGCAG TAGTC ACTTG AGGAT 120
TTTTT TTCCA ATTCT TTCTT TTTTG TTGTT AAAGC TGTAC TTCAG TGAAC AGAAA AATTG 180
CCAAG CAAAC TAATG GACTA TAAAG CGTAA TTTGA CTGTG TGGGA CTAAA CTACA GAGCC 240
TACTT GACCA GTGGA T 256

```

FIG.16L

AD4-4 T7F SEQUENCE

Sequence Range: 1 to 270

```

CATGT TTAAA AAAAA GTTGA TTGCT TCAAA TTA CT GCTAC TAACT TCAAG CTATG GGAGT 60
TTGGC AGTAG TCACT TGAGG ATTTT TTTTC CAATT CGTTT TCATT TTTGT TGTTA AAGCT 120
CGTAC TTCAG TGAGA CAGAA AAATT GCCAA GCTAA ACTAA TGGTC TATAA AAGCG TAATT 180
TGCAT GTGTG GGCAA AAAC TACAGA GCCTC AATTG CCACT GAGGT ATAGT ACAA GTTTT 240
AATAC ATTTT GTAAA TCAAA TTGAA AGAAA 270

```

FIG.16M

AD4-4 SEQUENCE

```

CATGTTTAAA AAAAGTTGA TTGCTTCAAA TTA CTGCTAC TAACTTCAAG CTATGGGAGT 60
TTGGCAGTAG TCACTTGAGG ATTTTTTTTC CAATTCGTTT TCATTTTGT TGTAAAGCT 120
CGTACTTCAG TGAGACAGAA AAATTGCCAA GCTAACTAA TGGTCTATAA AAGCGTAATT 180
TGCATGTGTG GGCAAAACT ACAGAGCCTC AATTGCCACT GAGGTATAGT ACAAAGTTT 240
AATACATTTT GTAAATCAAA TTGAAAGAAA 270

```

FIG.16N

AD16c-T7 SEQUENCE

```

TCTGC CCAGG CTGGT CTGAA ATTCC TGGGC TGAAG TGATC CTCCA GTCTT GGCCT CCCAA 60
AGTGC TGGGA TTACA GGCAT GAGCT ACTGA GCCTA GCCTT AATGA TTAAT TTTAG AGTGA 120
TGGCT TGTAC CTTCA AGACA CATAT AGATT GAGAC AGAAA ATTTC CATCG TCCCC GAGAA 180
AACT 184

```

AD16c-T7 PEP

```

          5   10   15   20   25   30   35   40   45   50   55   60
SSSLG LPKCW DYRHE LLSLA LMINF RVMAC TFKQH IELRQ KISIV PRKLC CMGPV CPVKI

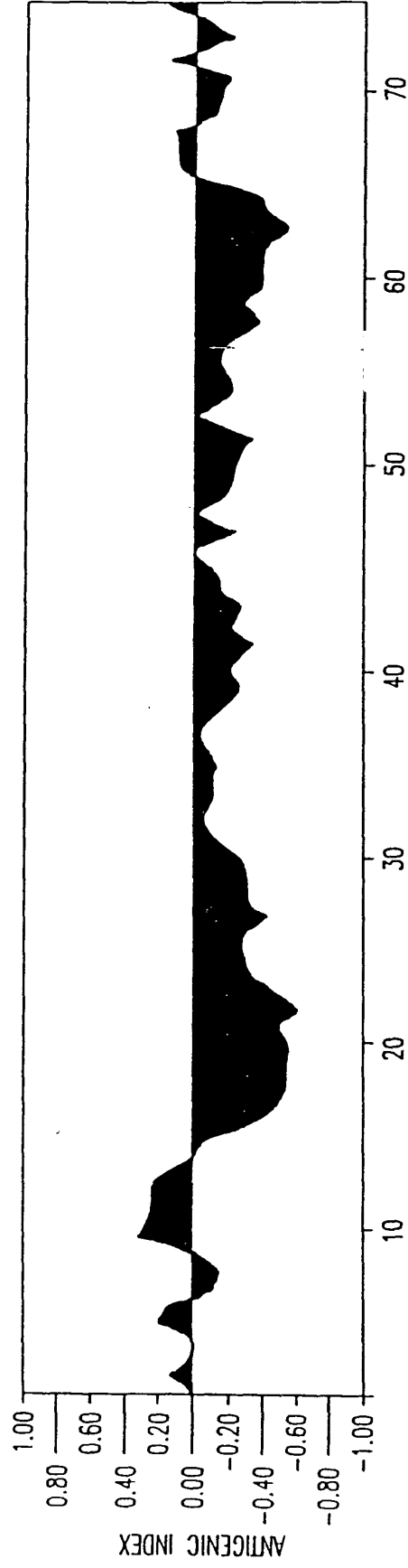
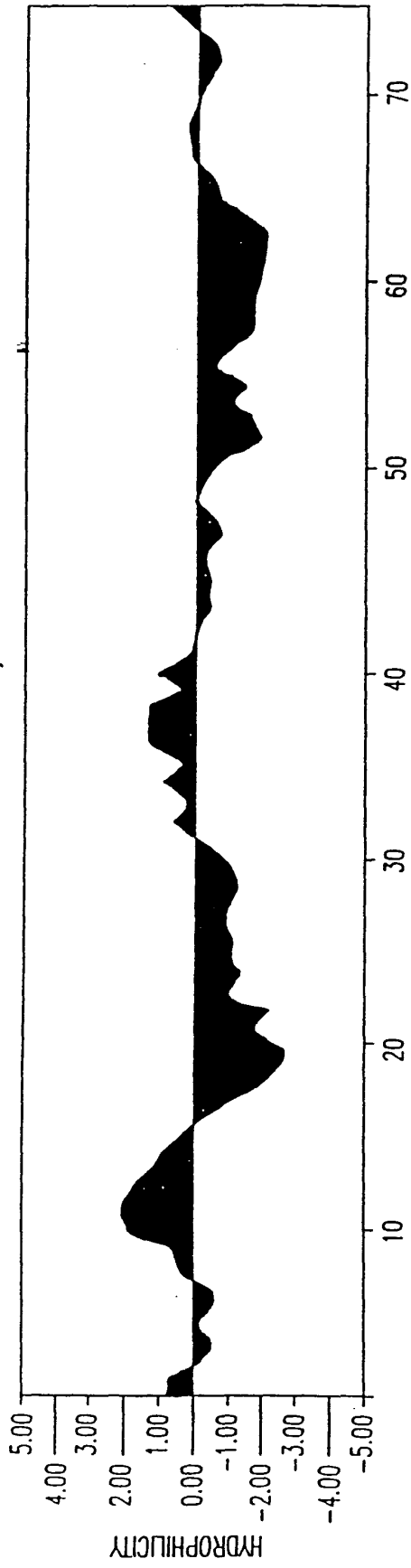
          65   70   75
ALLTI NGHCT WLPAS

```

FIG.16O

AD16c T7 HYDROPHILICITY WINDOW PLOT

HYDROPHILICITY WINDOW SIZE = 7 SCALE = Kyte-Doolittle



AD10-7 SEQUENCE

```

TTTTTTTTT GAGATGGAGT TTTGGCTCTT GTTGGCCAGG CTGGAGTGCA ATGGCGCAAT 60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCTGCCT CAGCCTCCCC 120
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTITAGTA 180
GAGATGGAGT TTAACCTCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC 240
TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCGCGGCCTC 300
TGCCTGGCTA ATTTTGTGG TAGAAACAGG GTTTCACCTG TGTGCCCCAA GCTGGTCTCC 360
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGGTCAGCC 420
GTGCTGGCC TTTTATTTT ATTTTITTA AGACACAGG GTACCACTCT TACCCAGGAT 480
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC 540
TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600
TTTATTTTIA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC 660
AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCTCCCGG GTTCAAGTTA TTCTCCTGCC 720
CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTITGTAT 780
TTTTAGTAGA GATGGGGTTT CACCATGTTT GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840
GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTGCTGACT CCACGCCGGC 900
CTATTTTAA TTTTGTITG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960
AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC 1020
AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCGGCTAATT TTTGTATTTT 1080
CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA 1140
CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200
GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320
TTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380
C

```

FIG.16R

AD16c-SEQUENCE

CCATTGTTAG GTTGCTCTT ACCTGTAAA ATCAGGAGCT GACAAGAAAT GCTTACCACA	60
AAAGGAGAAA TGCCAGTCTA GTTAACAGTC AAGGAGAGAA ATCAGGAAGA TTATGTGGGT	120
GGAGAAGTA GATGATGTGG CTGATGAGTG AGTGAGTGAG CAAGCCTCCG CCCAGCTGAA	180
GAAGGAGTCA GAACTGCCCT TTGTTCCCAA CTATTGGCG AACCCAGCC TTCCCTTTTA	240
TCTATACACC CACAGCAGAG GATTCAGCCC AGATGCAGAA TGGGGGCCCC TCCACACCCC	300
CTGCATCACC CCCTGCAGAT GGCTCACCTC CATTGCTTCC CCCTGGGAAC CTCCCTGTT	360
AGGGACCTTT CCCCGGACC ACACCTCTTT GGCAGTAGTT CAGAATGGTG ATGTGTCGGC	420
CCCTCTGCCA TACTAGAACA CCAGAAAGAC AAACGGTGA TGTGTGTCAG CTACAGTGAG	480
TCTAGAGCCG TCCTGTTTTT TTCTGTCCCG TCCCAAGCCA CCATGTCTCT TCGAGCCTCA	540
AAATGGGACC TATGCAGGAC CAGCGCCAG ATTCCAAGCC ATTTTCTTC ACTGGAGCAT	600
TTCCATTTAA TATGCAAGAG CTGGTACTCA AGTGAGAAT TCAGAACCCA TCTCTCGAG	660
AAAATGATTT CATTGAAATT GAACTGGACC GACAGAGCTC ACCTACCAAG AGTTGCTCAG	720
AGTGTTGTC TGTGAGCTGG GTGTTAATCC AGATCAAGTG GAGAAGATCA GAAAGTTACC	780
CAATACTCTG TTAAGGAAGG ACAAGGATGT TGCTCGACTC AAGATTTAG GAGCTGCAAC	840
TGTTCTGAT GATAGTAAA ATAATTTCT GTTCAGAAAT GCTGCATCAC ACTGACTGAA	900
AGGCCTTGCT ATACAGGAGA GCTTCAAAC TGACTTACTA ATGCAGCAGG GACTTTTATA	960
CTGAGTATAT GACAGTGTGC ATCACCTCTG GGCCAAGGAC AAGCCATGAT CTAAATGCCT	1020
CAGATGCCCC GGCCAGTCTG GTGCACTGCA TAGTATATAC GAACATCATT CTGCCAAGG	1080
TAGGAAGCCC CATGACCCCC AAGCAGTGGT GTCCACTCTT CCAAGCCTCT TGGTGCACAA	1140
TAAACCTTAT TGCTTGAAGC TTTGAACGAC TGTGAGAATG GTCTGGCGAG GACGAGAACG	1200
TGGAATTATA TGAGTGTCTT TTGTATCGA GAATGTAGAG AGTTCTCTGA AGACGACGAC	1260
TGAGAGAGAG CGGACGCTAT TTCTAGCCAC TCCTGTTGAC AGTGCACCTG AAGGGCTGGG	1320
ATGCGTTTTT CTGGTGTTC CATGCTCACA ACTCTGCTGA CATTGGGAAC TTATGAGAGA	1380
GGAAGACTCG GGAAAGCACA GATACTGGAC AGATGGATTG TGGTGTGGGG AAAGCACAGA	1440
TACTGGACAG ATGGTTCTAG TGTACTTGT GACTGTGAGG TTTCTATAA CATATTTATA	1500
AATGTTATC AGGTTCAAAA GTCTATAAGA ATACAGTTCC AGACTGAAT GCTTCGAAAT	1560
ACTTCGATGT TGGGAACCAA AAGAGCTTTC CCTCCCTCAC TTTTCTCTT GTAACACTCA	1620
TGACTGCTTC TCTGTCTCGA GTCATCTCTG CATTAACTCC CCTTGTGGT CACTAGAGGG	1680
CTCTCTGATG CTTCTAAGAC ACTGCTTTT ACATGCCACA CCCACCGGT AGAGACAGGG	1740
TCTCACTATG TGGCCAGGC TGGTCTCAA CTTCTGGCT TAAGTGATCG TCCTGTCTT	1800
CGCGCTCGGA AGAAAGTCGT GGGGATTACA GGTGTGAGCC ACCCGCCAG CCCCTCCCTT	1860
GTGTTTCAAC CAATCGGAAG TGAATTAAC TAGATGTAGT AACCTTTTTT TTCTTTGACT	1920
TCTAAAAAAG TTACAGTTTA CTAATAAAGT TAAGTCTGGT TCTGTCTAG AGGAAATAAA	1980
TTCACTATTA ATTCATGTCT TAAGTTACTT GGGTTAAAC ACTTTCAGCC ACCCAGATTA	2040
ATTAAGTGG AGCAGTGGAG CCCCTGGCTG GGGAGATGGG CCTCCAGAG AGCAGCTCCA	2100
GGCATGTTCT GGCTACACAG AGGCAAGCAA GGGACTGGTG TCTCTGGTGA GAGGTGGGT	2160
TGATGTATCT CTGTCTATG CTGGTCTCTC TTCTCCTTA TAAATCCTCC TGTGGTCACT	2220
GACTATCGTA TCGCAGTGAT CAGACTGCAC ATAGTACGGT TAGGCTGAGC TTAATGTCTT	2280
AATCATGTCA TTCGAGAGAA GACACGTTT GATTCATGCT TTGTGTAAT AATCAATCAA	2340
GGATTCTTTT TTTAGCTTTG TTGACGTGTA ATTCACCCCT CCTCCTCCAC TGCATATTTA	2400
AAGCATGTGT TCACACTGTG TGTATACATT CACTGCGATT TTTTCGTTG CTGCATTGCT	2460
TGGACTGTTT ATAACATCAC AAGTATTATT CAAATAAAT ATTAAGTGAC CGAAAAAAA	2520

FIG.16S

H REG GENE
[220] ————— GA ATTC TGggC TCAaG TGATC CClCtC aLgTC AGlCT CCCAA AGTGC TGGGA>
AD2-283 GA ACTCC TGACC TCAGG TGATC CGCCC GCCTC AGCCT CCCAA AGTGC TGGGA

H REG GENE	55	60	65	70	75	80	85	90	95	100		
[220]	TgACA	gGcTt	G-AG-	CC-A	-CCAc	ACcAg	gcccA	-TC-	AtCo-	G-tT	tTtOt	A-taA>
AD2-283	TTACA	AGCGT	GCAGA	CCGCA	CCCAG	ACGAT	TTTAA	TTCTT	AACNT	GCCAT	CCTCT	ACCCA

H ⁺ REG GENE	105	110	115	120	125	130	135	140
[220]	AGGaAa	AaAaa	ACcTT	AaaaT	tgltA	gCAAA	tacta	TGACA>
AD ² -283	AGTAC	AGACC	ACTTT	AGTGT	CCCTA	TCAAA	GGGGG	AGACA

FIG. 17

AD2 SP6F 110 115 120 125 130 135 140 145 150
[62] —AA ttc-t C-CtG cCTCA GCCtc gLGag ccGct GGgAT TACAG GcG>
EXONI AA GCCAA CTCAG ACTCA GCCAA CAGGT AAGTG GGCAT TACAG GAG

RAT PTP	605
[144]	<ACTC
AD2-2 T7	ACTC

RAT PTP 660 655 650 645 640 635 630 625 620 615 610
 [144] <tcT-o ggoAg aGggg GTTGA C—t tTGCT TTtGA taGaT GGT-c TagT- TTCac TTttg
 AD2-2 T7 AGTGT TTTAT TGCTA GTTGA CAAAG CTGCT TTtGA ATGCT GGTGG TTCTA TTCCT TTGAC

RAT PTP	710	705	700	695	690	685	680	675	670	665		
[144]	<aCA-T	aCAAT	AoTGg	aGatA	-aaaa	ToCcA	T-A-G	GgCag	T-GA	GGcA-	AgaaT	GTTtG
AD2-2 T7	TCATT	TCAAA	ATTGC	TGCCA	GTGTT	TTCAA	TGATG	GACAA	TCAGA	GGGAT	ATGCT	GTTAG

RAT PTP
[144]
AD2-2 T7

745 740 735 730 725 720 715
G Tg A-Agg taTTT TtAtT TaaaT gTgca gggTT
GTA ATACT CCTTT TTTCT TCTTT CTTTT TTTTT

HPTPAA

5
FVF cLII>
EVA SLIK

FIG. 17A

1-9aT7-3 3 140 145 150 155 160 165 170 175 180 185 190 195
 [206] ACcAC GCCCc GCTAA TlTTT GTATT TTTAG TAGAG AcdGG GTTTC dCCgT GTTgg cCAGG>
 AD2-283 ACAAC GCCCA GCTAA TATTT GTATT TTTAG TAGAG ATGGG GTTTC TCCAT GTTCA TCAGG

1-9a-T72 3 15 20 25 30 35 40 45 50 55 60 65 70
 [260] CTGGT cTgaA AlTCC TGggC TgAdG TGATC ClCCa GlCTL gGCCT CCCAA AGTGC TGGGA>
 AD2-283 CTGGT GTCGA ACTCC TGACC TCAGG TGATC CGCCC GCCTC AGCCT CCCAA AGTGC TGGGA

1-9a-T72 3 140 145 150 155 160
 [260] AG=AC AcA-l A-Tag AlTGa gaC-A gaAAA>
 AD2-283 AGTAC AGACC ACTTT AGTGT CCCTA TCAAA

FIG.17B

AD16c-SP6 5 10 15 20 25 30
 [344] -AGA- TcTCg CTC-I G-Tca CCCAG GCTGa AGTGC>
 AD2-2 SP6 AGAG TTTCA CTCTT GCTTG CCCAG GCTGG AGTGC

AD2-2 SP6 35 40 45 50 55 60 65 70 75 80 85
 [344] AgTGG CcCAA TClcG GCTCA CTGCg AgCTC C-dCC TCCCG gGlTC Actlc aTTCT CCTGC>
 AD2-2 SP6 AATGG CACAA TCCTG GCTCA CTGCA ACCTC CGCCC TCCCG AGCTC AAGAA CTCTT CCTGC

AD16c-SP6 100 105 110 115 120 125 130 135 140 145 150 155 160
 [344] CTCAG CCTC- TGAGl dGCTG GGAcT ACAGG CGCcC dCCAC AcGCc gCTAA TlTTT GTATT>
 AD2-2 SP6 CTCAG CCTCG TGAGC CGCTG GGATT ACAGG CGCGC GCCAC AAGCG ACTAA TATTT GTATT

AD16c-SP6
 [344] TTTGT AG>
 AD2-2 SP6 TTTGT AG

AD16c-SP6 140 145 150 155 160 165 170 175 180 185 190 195
 [206] ACcAC GCCCc GCTAA TlTTT GTATT TTTAG TAGAG AcdGG GTTTC dCCgT GTTgg cCAGG>
 AD2-283 ACAAC GCCCA GCTAA TATTT GTATT TTTAG TAGAG ATGGG GTTTC TCCAT GTTCA TCAGG

AD16c-SP6 200 205 210
 [206] aTGcT -CGA lCTCC TGA>
 AD2-283 CTGGT GTCGA ACTCC TGA

FIG.17C

H REG GENE 3610 3615 3620 3625 3630 3635 3640 3645 3650 3655 3660
 [118] —CC CC-aa gC-aG lGTta aTccl GG-cT A-CT GlgTG AGcTG AccTC AagcA CaGGt>
 AD3-4 CC CCTGT TCTTG GGTGG GTTTG GGTAT ATTCT GGTG AGATG ATATC ATTGA CCGGG

H REG GENE 3670 3675 3680 3685 3690 3695 3700 3705 3710 3715 3720
 [118] GAAGG Cagag aaTcc A-Tcc aCC-T gTTTC TgTTc TCCcT gCtTA gctcc AGGga TgGAA>
 AD3-4 GAAGG CGCTT TGTGA AGTAG GCCTT ATTTC TCTTG TCCTT TCGTA CAGGG AGGAT TTGAA

H REG GENE 3725 3730 3735 3740 3745 3750 3755 3760 3765 3770
 [118] cTgGg Actgg GaT-a gAgga aaG-g TGAAC TC-cT CA-lT aagga aATgG aTG>
 AD3-4 GTAGT AGAAC GCTGT TACTC CCGTC TGAAC TCAGT CACGT GGCTT TATCG TTG

FIG.18

WPO3-5 T7 5 15 20 25 30 35 40 45 50
 [90] GATCC aAGCT acGTA -CgcG TgcAT GCAcg lCaTa gcTcT TCTAT AGTGT CAC>
 AD3-4 221 GATCC GAGCT CCGTA CCAAG TTGAT GCATA GCTTG AGTAT TCTAT AGTGT CAC

18-4T7 155 150 145 140 135 130 125 120 115 110 105
 [362] <gTATg GgCcc gATAg —c-l TAT-l TAgcC TTTAG AGCAC ACTGG CgGCC GTTAC TAGTG
 AD3-4 221 ATATA GACAA TATAA CAATA TATTG TATAC TTTAG AGCAC ACTGG CAGCC GTTAC TAGTG

18-4T7 100 95 90 85 80 75 70 65 60 55 50 45
 [362] <GATCC GAGCT CCGTA CCAAc TTGAT GCATA GCTTG AGTAT TCTAT AGTGT CACcT -aAaT
 AD3-4 221 GATCC GAGCT CCGTA CCAAG TTGAT GCATA GCTTG AGTAT TCTAT AGTGT CACTA ATAGT

FIG.18A

G2A-EP T7 20 25 30 35 40 45 50 55
 [148] ——— CTT AaTA- gAlAg ctaCT TA— AAAla AcTTA CaC-A cT— GTtTt>
 AD3-4 SPF CTT ACTAC CAGAC AACCT TAGCC AAACC ATTTA CCCAA ATAAA GTATA

G2A-EP T7 60 65 70 75 80 85 90 95 100 105 110
 [148] aGag- T-G— cTTGA AAaCT aLCtg AtcAG AcATA GTAlt GaAAc cAAtG A—At AcATT>
 AD3-4 SPF GGCGA TAGAA ATTGA AACCT GGCGC AATAG ATATA GTACC GCAAG GAAAG ATGAA AAATT

G2A-EP T7 115 120 125 130 135
 [148] AT-At aAAG- -TAA- A-gGa AAGGA -gAA>
 AD3-4 SPF ATAAC CAAGC ATAAT ATAGC AAGGA CTAA

AD3-4 215 210 205 200 195 190 185 180
 [182] ——— <CT ATAAa GgTcG TTG— TcaaC gaToA AGCAc tLGAc
 H REG GENE CT ATAGA GATTG TTGAT TTGCC TCTTA AGCAA GAGAT

AD3-4 175 170 165 160 155 150 145 140 135 125
 [182] <TgAgt tCAG- aCcGg A-Gta aCAG- CgttC TacTA CTTCa -aaTc cTC-C CTGCg aaAgG
 H REG GENE TCATT GCAGC TCAGC ATGGC TCAGA CCAGC TCATA CTTCa TGCTG ATCTC CTGCC TGATG

AD3-4 120 115 110 105 95 90 85 80 75 70 65 60
 [182] <caaga Gaaal AagGC ClAct TAAGc gC-CT TccCC cgtAA atgAt atcaT CTcaa CCaGA
 H REG GENE TTTCT GTCTC AGAGC CAAGG TAAGA TCTCT TTTCC ACCAA CCAAC TCTTT CTAGC CCTGA

AD3-4 55 50 45 40 35 30 25 20 15 10
 [182] <AlA-T aCcCa aaccC CCCAA GaAcA gGGGa ggAaa aGAAA AAAAA AAAAA
 H REG GENE AGACT TCACT CTATC CCCAA GCATA CCGGT CTA CTACT TGAAA AAAAA AAAAA

FIG.18B

AD2-2 T7		535	530	525	520	515	510	505	500	495
[110]	—————	<CAGAA	AAcTa	GCTAc	aC-AA	tgcAt	TGGTC	TATcA	tgltA	aAAcg
AD4-4 T7F		CAGAA	AAATT	GCCAA	GCTAA	ACTAA	TGGTC	TATAA	AAGCG	TAATT

AD2-2 T7	490	485	480	475	470	465	460		
[110]	<TGCAT	-T—	a GaCAc	AAA-T	ACAaA	aacCA	TG—A	-AacA	aGCcA
AD4-4 T7F	TGCAT	GTGTG	GGCAT	AAACT	ACAGA	GCTCA	TGCTA	GAGTA	TGCAA

1-9a		145	140	135	130	125	120	115	110		
[142]	—————	<AA	-TTGg	gTAc-	-Cggg	cccCc	cCTA-	gAggT	cgAcG	gTAT-	cGA-T
AD4-4 T7F		AA	GTTGA	TTGCT	TCAAA	TTTCT	GCTAC	TAAC	TCAAG	CTATG	GGAGT

1-9a	105	100	95	90	85	80	75	70	65	60	55	50
[142]	<aaGct	lGTAt	cgAaT	TccGG	AcTTT	gcTT-	—TT	gGTTT	TCcTT	Tcctg	TGaaA	AgGtT
AD4-4 T7F	TTGGC	AGTAG	TCACT	TGAGG	ATTTT	TTTTT	CAATT	CGTTT	TCATT	TTTGT	TGTTA	AAGCT

1-9a	45	40	35	30	25	20	15	10		
[142]	<gGTltt	TaaAG	TGAG-	-AtAc	ActTT	lCC—	GtagA	ACaAg	TGtTC	TAT
AD4-4 T7F	CGTAC	TTCAG	TGAGA	CAGAA	AAATT	GCCAA	GCTAA	ACTAA	TGGTC	TAT

FIG.19

H REG GENE		5	10	15	20	25	30	35	40	45
[278]	-----g	AATTC	CTGGG	CTcAA	GTGAT	CCTCt	coTgT	coGtC	TCCCA	AAGTG>
AD16C-T7-A		A AATTC	CTGGG	CTGAA	GTGAT	CCTCC	AGTCT	TGGCC	TCCCA	AAGTG

H REG GENE	50	55	60	65	70	75	80	85	90	95	100	105
[278]	CTGGG	ATgAC	AGGCt	TGAGC	cACco	coCCo	gcCCo	TcATc	AgTtL	TTaTA	tAaAG	-aaaa>
AD16C-T7-A	CTGGG	ATTAC	AGGCA	TGAGC	TACTG	AGCCT	AGCCT	TAATG	ATTAA	TTTTA	GAGTG	ATGGC

H REG GENE	110	115	120	125	130	140	145	150	155	160		
[278]	aaaaA	CCT-t	A--aA	Attgt	TA-gG	caaAt	AaLGA	cAAaT	TgtAa	ta-La	tattc	tLACa>
AD16C-T7-A	TTGTA	CCTTC	AAGCA	ACATA	TAGAG	TTGAG	ACAGA	AAATT	TCCAT	CGTCC	CGAGA	AAACT

H REG GENE	165	170	175	180	185	190	195	200	205	210	215	220
[278]	tTtCa	-gATt	tttAt	ttTtT	aaaCT	GalAA	GAatt	gatTA	aTAAa	TAaAA	tTtAG	tAT-->
AD16C-T7-A	GTGCT	GCATG	GGCCC	CGTGT	GCCCT	GTGAA	GATCG	CCCTA	TTAAC	TATAA	ATGGG	CATTG

H REG GENE	225	230	235	
[278]	t-aA-	-tCtG	t-clt	TTaA>
AD16C-T7-A	CACAT	GGTtG	CCAGC	TTCA

FIG.20

AD16C
[266]
Human-PTP

5 10 15 20
aACgt TlcGA aCCTa tCgTg>
TACTG TGTGA GCCTG ACCTC

AD16C 25 30 35 40 45 50 55 60 65 70
[266] AAG-c -ccGA TTtTA GAgtT aatAc -ggGT -gC- lTcAA GggA- acggg gCTaT -ga->
Human-PTP AAGCA CAGGA TTCCA GAAAT GGAAG GATGT GCCTT GTGAA GACAA GTTCT CCTTT GTCTG

AD16C 75 80 85 90 95 100 105 110 115 120 125 130
[266] gAAGT -tllc tACgg GgaGC -aTG GAAAt TllcT GTCTc aAlaT GtgCt tGaAg gTACA>
Human-PTP CAAGT TCAAA AACTA GAGGC ACCTG GAAAA TACAT GTCTA GAACT GATCC AGCAA TTACA

AD16C 135 140 145 150 155 160 165 170 175 180 185 190
[266] ACcGt aTcTA AAATT AAtCa tt-aa ggCTa ggCtc agtAg CTCTg CCTGt -a-aT CcCag>
Human-PTP ACGGA GTCAA AAATT AAACC GGACC ATCTC TCCAA CTCAA CTCAA CCTGG ACACT CTCTT

AD16C 195 200 205 210 215 220 225 230 235 240
[266] CaC-t tTcgG gagGC Caa- gAcTg gaggA TcacT TcAg- ccCag gAa-t TTcaG AcgCc>
Human-PTP CTCTG CTGAG TTTGC CTTGT TAATC TTCAA TAGTT TTACC TACCC CAGTC TTTGG AACCT

AD16C-T7-A 205
[33] VPCE Dr>
HPTPAA VPCE DK

RPTP AA 115 120
[33] SgSLf LyKsW D>
Translatio SSSLG LPKCW D

FIG.20A

ALIGNMENT OF AD16C-SP6 cDNA WITH AD2-2 SP6 cDNA

AD2-2 SP6	40	45		50	55	60	65	70	75	80	85	90
[362]	CTtGC	T-TG-	—CCC	AGGCT	GgAGT	GCAoT	GGCoC	AATCc	tGGCT	CACTG	CoAcC	TCCcC>
AD16C-SP6-	CTCGC	TCTGT	CACCC	AGGCT	GAAGT	GCAGT	GGCCC	AATCT	CGGCT	CACTG	CGAGC	TCCAC

AD2-2 SP6	95	100	105	110	115	120	125	130		135	140	145
[362]	CTCCC	GoGcT	CAaga	acTTC	TCCTG	CCTCA	—GCC	TC-G-	—TG	AGccG	CTGGG	ALTAC>
AD16C-SP6-	CTCCC	GGGTT	CAC TT	CATTC	TCCTG	CCTCA	CTGCC	TCAGC	CTCTG	AGTAG	CTGGG	ACTAC

AD2-2 SP6	150	155	160		165	170	175	180	185
[362]	AGGCG	CgCgC	CA-CA	oG—	-CgaC	TAA-T	aTTTG	TATTT	TT-GT AG>
AD16C-SP6-	AGGCG	CCCAC	CACCA	CGTCC	CCTGC	TAATT	TTTTG	TATTT	TTAGT AG

AD2-283	50	55	60	65	70	75	80	85	90	95	100	105
[374]	CCoTG	TTcoI	CAGGc	TGGTg	TCGAo	CTCCT	GACCT	CGTGA	TCCGC	CCGCC	TcoGC	ClCCC>
AD16C-SP6-	CCGTG	TTGGC	CAGGA	TGGTC	TCGAT	CTCCT	GACCT	CGTGA	TCCGC	CCGCC	TTGGC	CACCC

AD2-283	110	115	120	125	130
[374]	AAAGt	G-cTG	GGATT	ACAoG	CGTGC>
AD16C-SP6-	AAAGA	GTTTG	GGATT	ACAGG	CGTGC

FIG.20B

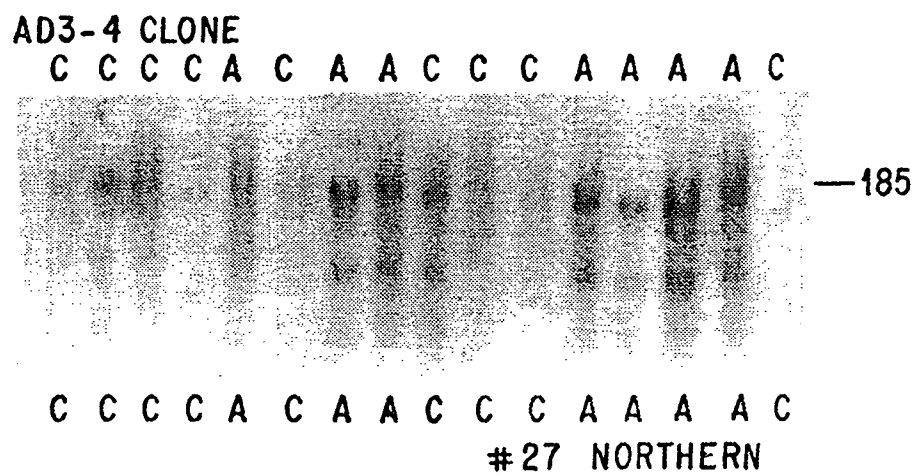
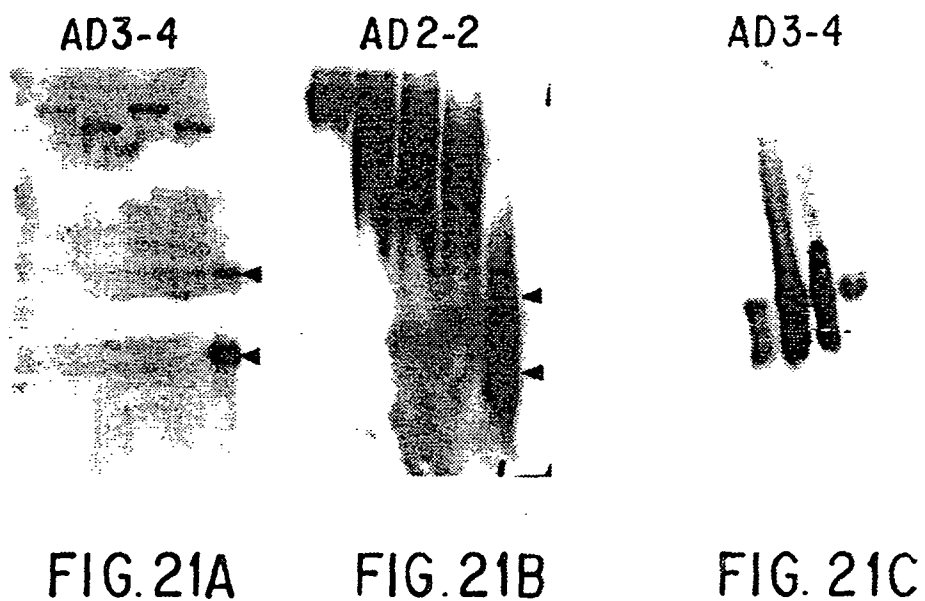


FIG. 21D

G2-2Pst-M13F SEQUENCE

Sequence Range: 1 to 251

```
TGCAG CAATG GCAAC AACGT CTGCA AACTA TTAAC TGGCG AACTA CTTAC TCTAG CTTCC 60
CGGCA ACAAT TAATA GACTG GATGG AGGCG GATAA AGTTG CAGGA CCACT TCTGC GCTCG 120
GCCCT TCCGG CTGGC TGGTT TATTG CTGAT AAATC TGGAG CCGGT CGAGC GTGGG TCTCG 180
CGTAT CATTG GAGCA CTGGG GCCAG ATGGT AAGCC CTCCG TATCG TAGTT ATCTC ACAGC 240
AGGGA GTCAG G
```

FIG.22

G2-2Pst-M13R SEQUENCE

Sequence Range: 1 to 242

```
TGCAG GAGCG GGGAG GCACG ATGGC CGCTT TGGTC CGGAT CTTTG TGAGG AACCT TACTT 60
CTGTG GTGTG ACATA ATTGG ACAA CTACC TACAG AGATT TAAAG CTCTA AGGAA ATATA 120
AAATT TTTAA GTGTA TAATG TGTTA AACTA CTGAT TCTAA TTGTT TGTGT ATTTT AGATT 180
CCAAC CCTAT GGAAC CTGAT GAATG GGAGC CAGTG GTGGA ATGCC TTTAA TGAGG AAACC 240
TG
```

FIG.22A

G2-2Pst1-EcoR1-M13F SEQUENCE

Sequence Range: 1 to 208

```
TGCAG CAATC TTTCT TATAT ACATG CTAA TAGAT AGCTA CTAA AATAA CTTAC ACACG 60
TTTA GAGTT GCTTG AAAAC TATCT GATCA AGACA TAGTA ATTGA AACCA ATGAA TACAT 120
TATAT AAAGT AAAGG AAAGG AGAAG AGAGG AAAGG GAGGG GAAGA GGAGA GGGAG GGACA 180
AGCGA GAAAG GAAAG GGAAG GGAGA AAA
```

FIG.22B

Gen2-2Pst1-EcoR1-M13R SEQUENCE

Sequence Range: 1 to 152

```
CTCAC TAAAG GGATC AAGGA ATAAT TTTGA ATTC AAGTC TTACA TTAA TAAAT ACATT 60
CATAA GGCTA TAACT ACCAT ACGTT GTGAT TTCTC TGATT AATTT AAAAA TAAAT TAAAA 120
CCTGG AAAGA ATTTT ACCAT TCTAG GAAGC CA 152
```

FIG.22C

G2-2Pst1-EcoR1-T7 SEQUENCE

Sequence Range: 1 to 338

```
AATCT ATCTT ATATA CATGC TTAAT AGATA GCTAC TTAA ATAAC TTACA CACGT TTTAG 60
AGTTG CTTGA AACT ATCTG ATCAA GACAT AGTAA TTGAA ACCAA TGAAT ACATT ATATA 120
AAGTA AAGGA AAGGA GAAGA GAGGA AAGGA GGGGA GAGGA GAGGA GGACA AGCGA GAAAA 180
GGAAG GGAAG GGAGA AAAAG GGGGA AAGGG AGGTA GAGAG AGAGA GAAAA AGTGC TGGTC 240
ATATA GTAAG TGTAC ATTTT AACTT TTAA GAAAC TACCC TACTC TATTC CAGAG TGATT 300
GTACA TGTGC ATTTT ACTGC ATTAT AGAGA TCATT TTC 338
```

FIG.22D

G5dPst-M13R SEQUENCE

Sequence Range: 1 to 169

```
TGCAG GAGTG GGGAG GCACG ATGGC CGCTT TGGTC CGGAT CTTTG TGAAG GAACC TTACT 60
TCTGT GTGTG ACATA ATTGG ACAA CTACC TACAG AGATT TAAAC GTCTA AGGTA AATAT 120
AAAAT TTTTA GTGTA TAGGT TAAAC TACTG ATTCT AATGT TGTGT ATTT 169
```

FIG.22E

G5d Pst-T71 SEQUENCE

Sequence Range: 1 to 209

```

CCCCG GGCTG CAGCA ATGGC AACAA CGTCT GCAAA CTATT AACTG GCGAA CTCAT TCATC 60
TAGCT TCCCG GCAAC AATTA ATGAC TGGAT GGAGG CCGAT AAAGT TGCAG GACCA CTTCT 120
CGCGT GGCCC TTCCG GCTGG CTGGT TTATT GCTGA TAATT GAGCG TGCGA GTGGC TCGCG 180
TATCA TTCGC GACAT GGGCC AGTAG GTAC                                     209

```

FIG.22F

G5dPst1-EcoR1-SP SEQUENCE

Sequence Range: 1 to 272

```

CTTGC CCTTC ATGGA GTCAT ACAGC CGATC AGCAA AATGC AGGGG CTTGT TCTGA ATGCA 60
CTGAA CCAGG TTCAG GAAAG CATTI TCCAG GTCTC CTTTA ACCTC TTTCC TGATG CTTTC 120
CAACA TGTC AAGG GCTGT AACTC TTGTA CCTAT CAAAT ACTTT CTGGA GGTGG GGACA 180
CGCTC CGCTC GGTCA TGATG CTGAT CCACT TGGGA ACATC AGTTC TTTCC TCTTC ACTCC 240
AGCTG CATAG AGATC CGAGG ACTCT TGGTC AA                                     272

```

FIG.22G

G5dPst1-EcoR1-l7 SEQUENCE

Sequence Range: 1 to 278

```

ACGGC CCAGC TTCCT TCAAA ATGTC TACTG TTCAC GAAAT CCTGT GCAAG CTCAG CTTGG 60
AGGGT GATCA CTCTA CACCC CCAAG TGCAT ATGGG TCTGT CAAAG CCTAT ACTAA CTTTG 120
ATGCT GAGCG GGATG CTTTG AACAT TGAAA CAGCC ATCAA GACCA AAGGT GTGGA TGAGG 180
TCACC ATTGT CAACA TTTTG ACCAA CCGCA GCAAT GACAC GAGAC AGGAT ATTGC CTTGG 240
CCTAC CAGAG AAGGA CCAAA AAAGG AACTT GCATC ACA                                     278

```

FIG.22H

ALIGNMENT OF G2-2Pst1 with HUMAN REG GENE (1)

H REG GENE	3405	3410	3415	3420	3425	3430	3435	3440	3445	3450	3455
[228]	—AG CAATa GCAA- -AgGa aaGgA AAC-A aTAtt TaGC- AA-gg tTTAt TCTtc CTTtg>										
G2-2Pst-M13F	AG CAATG GCAAC AACGT CTGCA AACTA TTAAC TGGCG AACTA CTTAC TCTAG CTTC										

H REG GENE	3465	3470	3475	3480	3485	3490	3495	3500	3505	3510
[228]	tGtCA gCAIt TctgA GtgTG cAcac AGGCc cAgTg A=ITc CAIG- -LATI- TtTGa-G-T-G>									
G2-2Pst-M13F	CGGCA-ACAAT TAATA GACTG GATGG AGGCG GATAA AGTTG CAGGA CCACT TCTGC GCTCG									

H REG GEN3515	3520	3525	3530	3535	3540	3550	3555	3560	3565	3575	3580
[228]	aCCac TgCct CTGtC TGG-c ccTtC CccAT AgAaC cGccG CtGGT gGAGC GTGGG TCcCt>										
G2-2Pst-M13F	GCCCT TCCGG CTGGC TGGTT TATTG CTGAT AAATC TGGAG CCGGT CGAGC GTGGG TCTCG										

EXON						20	25	30	35	40	
[124]	_____					C	TGGca	CtGG-	aG-ca	GTGGG	TCcCt>
G2-2Pst-M13F						C	TGGAG	CCGGT	CGAGC	GTGGG	TCTCG

H REG GENE	3585	3590	3595	3600	3605	3610	3615	3620	3625	3630
[228]	gGTcT CcTaC aAGtC CTGGG G-CA- tTGG- -AGCC CcaaG cA-G T-GTT A-aTC ctgGC>									
G2-2Pst-M13F	CGTAT CATTG GAG Q CTGGG GCCAG ATGGT AAGCC CTCCG TATCG TAGTT ATCTC ACAGC									

EXON5	45	50	55	60	65	70	75	80	85	90	95
[124]	gGTcT CcTaC aAGtC CTGGG G-CA- tTGG- -AGCC CcaaG cA-G T-GTT A-aTC ctgGC>										
G2-2Pst-M13F	CGTAT CATTG GAG Q CTGGG GCCAG ATGGT AAGCC CTCCG TATCG TAGTT ATCTC ACAGC										

H REG GENE3635	3640
[228]	ActGt GTqAG>
G2-2Pst-M13F	AGGGA GTCAG

EXON5	100	105
[124]	ActGt GTqAG>	
G2-2Pst-M13F	AGGGA GTCAG	

FIG.23

ALIGNMENT OF G2-2Pst with HUMAN REG GENE (2)

```

H REG GENE 3155 3160 3165 3170 3175 3180 3185 3195      3200
[ 194 ]  —AG GAGac tTGtG GtA-a AaatC lGCTg cTGtA cTGcT CaTT- TG-GG AACCT TA-gT>
G2-2Pst-M13R AG GAGCG GGGAG GCACG ATGGC CGCTT TGGTC CGGAT CTTTG TGAGG AACCT TACTT

H REG GEN3210 3215 3220 3225 3230 3235 3240 3245 3250 3255 3260 3265
[ 194 ]  aTact aaaTa ATATA A-Tat ATcAA CaACT aAtgG tCagc cAATG CTaTg cTG-g ATATg>
G2-2Pst-M13RCTGTG GTGTG ACATA ATTGG ACAA CTACC TACAG AGATT TAAAG CTCTA AGGAA ATATA

H REG GENE 3270 3275 3280 3285 3290 3295 3300 3305 3310 3315 3320
[ 194 ]  AgggT ccT-g GgccA cAAaG acaaA AAaT- CaGga aCcAc TT-TT TaaGT gagaT ActTT>
G2-2Pst-M13RAAATT TTTAA GTGTA TAATG TGTTA AACTA CTGAT TCTAA TTGTT TGTGT ATTTT AGATT

H REG GEN3325 3330 3335 3340 3345 3350 3355 3360 3365 3370 3375
[ 194 ]  gggTC lCTgT -cAAa tTcAT aAcac tTAtt tctTG GTGGA ATaCa gTTAA TGAG>
G2-2Pst-M13RCCAAC CCTAT GGAAC CTGAT GAATG GGAGC CAGTG GTGGA ATGCC TTTAA TGAG

G2-2Pst-Ma3F 150 155 160 165 170 175 180 185 190 195
[ 130 ]  ———TA aATcT GgaGC cGG— -TcGA GC-GT GGGTC lCgcG TaTCa TlCgA GcaCT>
EXON5      TA GAACC GCCGC TGGCA CTGGA GCAGT GGGTC CCTGG TCTCC TACAA GTCCT

G2-2pst-M13F 200 205 210 215 220 225 230 235 240 245 250
[ 130 ]  GGGGC —caG A-tgg tAAGC ccTcc gtATC gToGt TA-Tc TcacA GCagG gagTC AgG>
EXON5      GGGGC ATTGG AGCCC CAAGC AGTGT TAATC CTGGC TACTG TGTA GCCTG ACCTC AAG

```

FIG.23A

ALIGNMENT OF G2-2PST-ECOR1-T7 WITH HUMAN REG GENE

H REG GENE		335	340	345	350	355	360	365
[132]	_____	AT	AGATA	lCTAC	TTlAl	lCgAl	TTAaA	lLCTG -TTTA>
G2-2PST-ECOR1 T7		AT	AGATA	GCTAC	TTAAA	ATAAC	TTACA	CACTG TTTTA

H REG GENE	370	375	380	385	390	395	400	405	410	415	
[132]	-GTa	lTTlA	lLA-T	ATlTt	gTlA-	A-T-	ccAlT	TG-lc	CCAAT	lCATA	lAcT- TAT>
G2A-EP T7	GAGTG	CTTGA	AAACT	ATCTG	ATCAG	ACATA	GTAAT	TGAAA	CCAAT	GAATA	CATTA TAT

RAT PTP		740	735
[82]	_____	<TqAAq	qlATT
G2-2PST-ECOR1-M1			TAAAT
ACATT			

RAT PTP	730	725	720	715	710	705	700	695	690	685		
[82]	<-Tlt	atlTA	-AAtg	lgCA-	ggGTT	-acA-	TaCaa	TaATg	gAgaT	AAAAA	TAcca	TAggg
Gen2aEP-Ma	CATAA	CGCTA	TAACT	ACCAT	ACGTT	GTGAT	TTCTC	TGATT	AATTT	AAAAA	TAAAT	TAAAA

RAT PTP	68675	670	665	660	655	
[82]	<CgaGG	caAGA	ATgTT	-lg	TCTAG	GAAG
G2-2PST-ECOR1-M1	CCTGG	AAAGA	ATTTT	ACCAT	TCTAG	GAAG

FIG.23B

Human-PTP		270		280	285	290	295	300	305	310	315	
[166]	—	AcCTG	GtGct	gTgCT	cAC-C	cAGgc	cgaGG	gtgC-	cTTtg	TgGcC	T-cAc tGAtt>	
G5dPst-t		AACTG	GCGAA	CTACT	TACTC	TAGCT	TCCGG	CAACA	ATTAA	TAGAC	TGGAT GGAGG	
Human-PTP	320	325	330	335	340	345	350	355		360	365	370
[166]		aaG-g	AgAGT	gGCAt	GAtgA	CTTCa	atG-T	CtG-g	aTT—	GGC—	-CTcc	aTgAc ccCaa>
G5dPst-t		CGGAT	AAAGT	TGCAG	GACCA	CTTCT	GCGCT	CGGCC	CTTCC	GGCTG	GCTGG	TTTAT TGCTG
Human-PTP	375	380	385	395	400	405	410	415	420	425	430	435
[166]		AaAgA	aCcGc	cGCtG	GgGAG	CGTGG	GTCcC	tgGTc	TCcTa	caAGt	cCTGG	GG-CA -tTGG>
G5dPst-t		ATAAA	TCTGG	AGCCG	GTGAG	CGTGG	GTCTC	GCGTA	TCATT	GCAGC	ACTGG	GGCCA GATGG
Human-PTP		440	445	450	455	460	465	470				
[166]		—AGC	CCcaa	GcA—	GTGtT	aATCc	tggCt	ACtGt	GtG-A	-GcC>		
G5dPst-t		TAAGC	CCTCC	GTATC	GTGGT	TATCT	ACACG	ACGGG	GAGTA	CGGC		

FIG.23C

H REG GENE		80	85	90	95	100	105	110	115		
[158]	—————	AG	GC-Cc	ATcat	CagTT	T—T-	totAT	aaaga	aaAAa	aAACC	TTAaa>
G5dPst-M		AG	GCACG	ATGGC	CGCTT	TGGTC	CGGat	CTTTG	TGAAG	GAACC	TTACT

H REG GENE	120	125	130	135	140	145	150	155	160	165	170	175	
[158]		atTGT	taGgc	AaATA	cTatG	ACAAA	-Ttgt	aAlAt	AtATT	cttAC	aTtTc	AGaT-	-tTtT>
G5dPst-M		TCTGT	GTGTG	ACATA	ATTGG	ACAAA	CTACC	TACAG	AGATT	TAAAC	GTCTA	AGGTA	AATAT

H REG GENE	180	185	190	195	200	205	210	215	220	
[158]	AtLlT	TTaaA	cTGTA	TAGaa	TtgAt	TaATa	AaTaa	AAT-I-I-	aGT	ATT>
G5dPst-M	AAAAT	TTTTA	GTGTA	TAGGT	TAAAC	TACTG	ATTCT	AATGT	TGTGT	ATT

G5dPst-t		125	130	135	140	145	150	155	160	165		
[118]	—————	TA	aAlCt	GgaGC	cGG—	-T-GA	GC-GT	GGGTC	tCgcG	ToTCa	TlgcA	GcaCT>
EXON5		TA	GAACC	GCCGC	TGGCA	CTGGA	GCAGT	GGGTC	CCTGG	TCTCC	TACAA	GTCCCT

G5dPst-t	170	175	180	185	190	195	200	205	210	215	220	
[118]	GGGGC	—caG	A-tgg	TAAGC	ccTcc	gtATC	gTGGI	TA-Tc	T-acA	—cG	ACggg	gAGtA>
EXON5	GGGGC	ATTGG	AGCCC	CAAGC	AGTGT	TAATC	CTGGC	TACTG	TGTGA	GCCTG	ACCTC	AAGCA

G5dPst-t	
[118]	C-CG>
EXON5	CAGG

FIG.23D

FIG. 24A

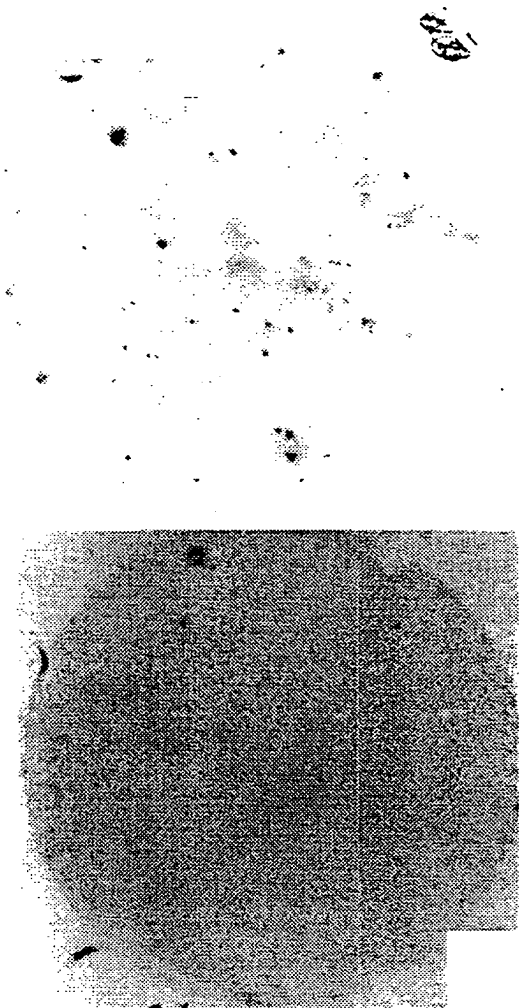


FIG. 24B

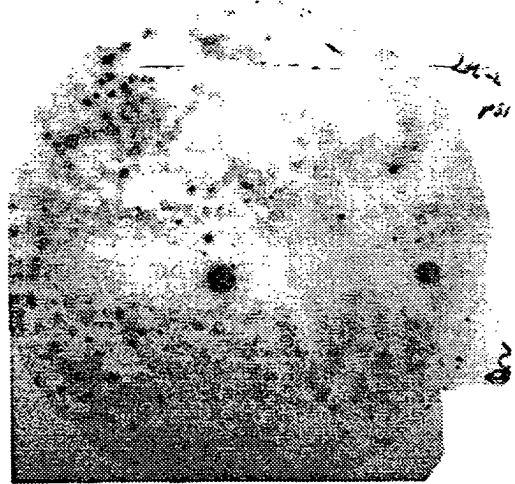


FIG. 24C

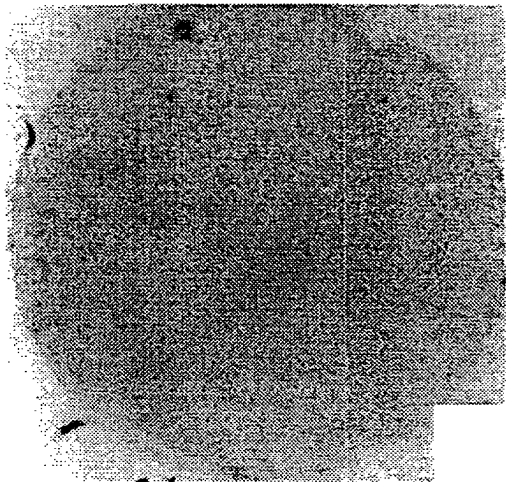
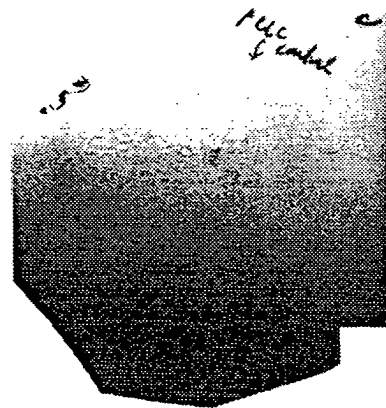


FIG. 24D



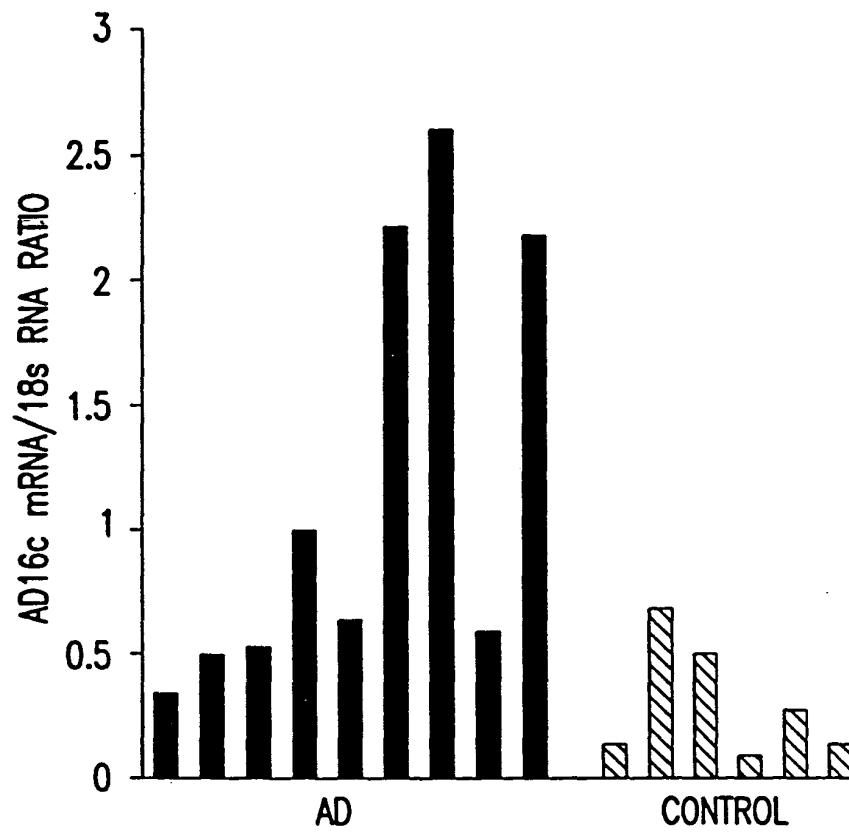


FIG.25A

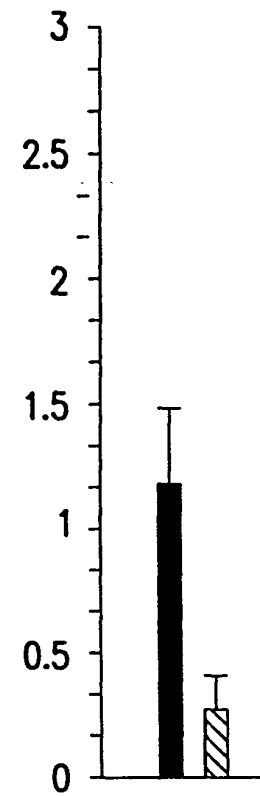
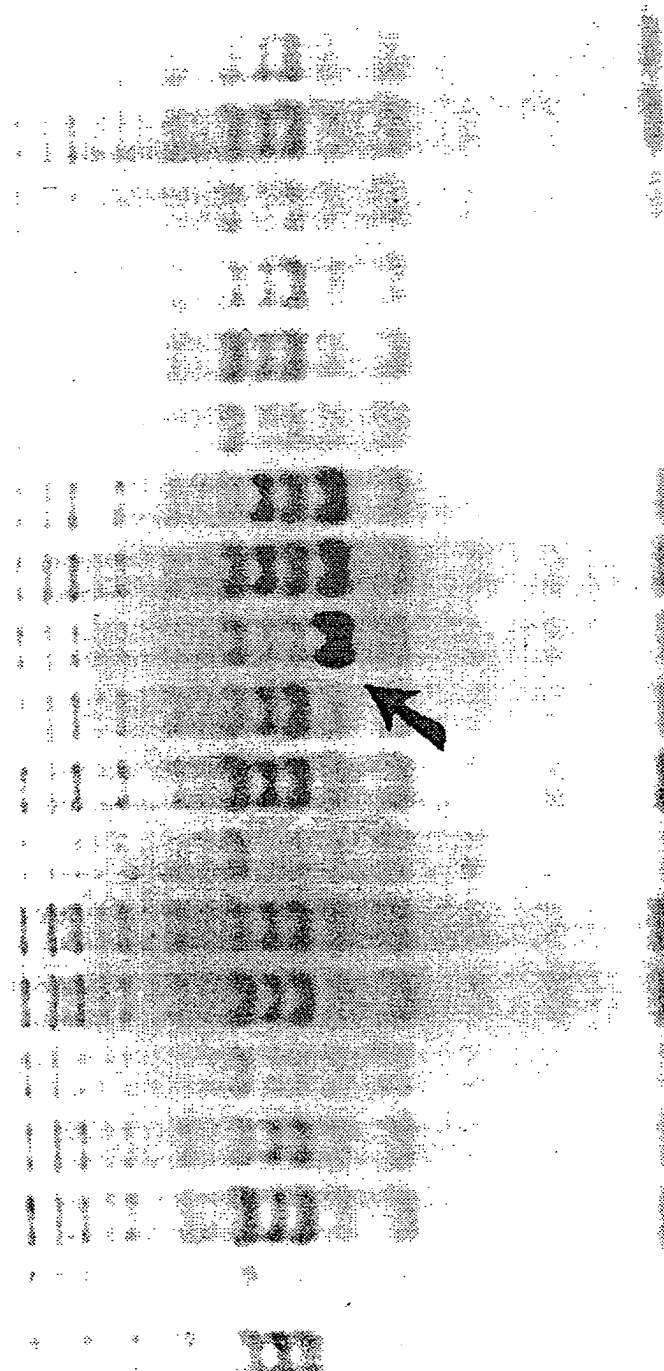


FIG.25B

18



Prot. Gel. 18 3/17/94/WB

FIG. 26

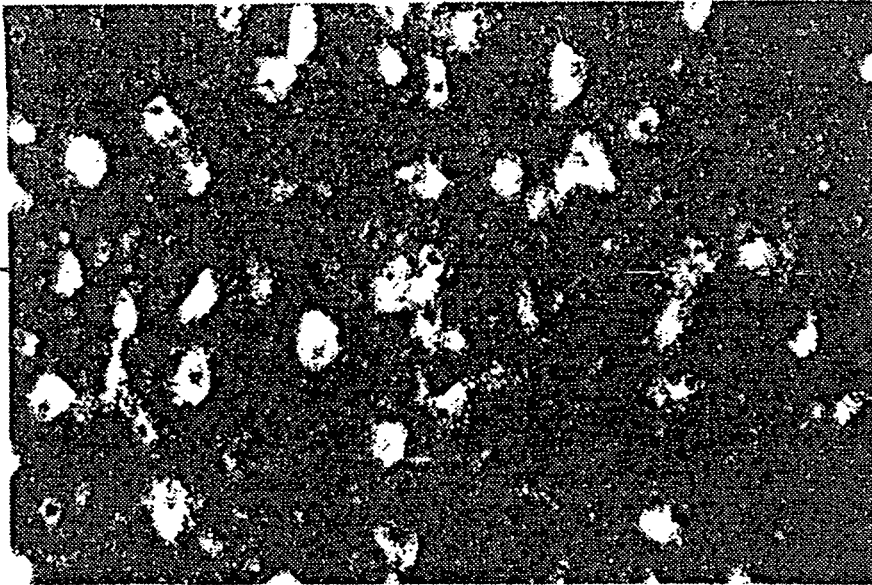


FIG. 27A

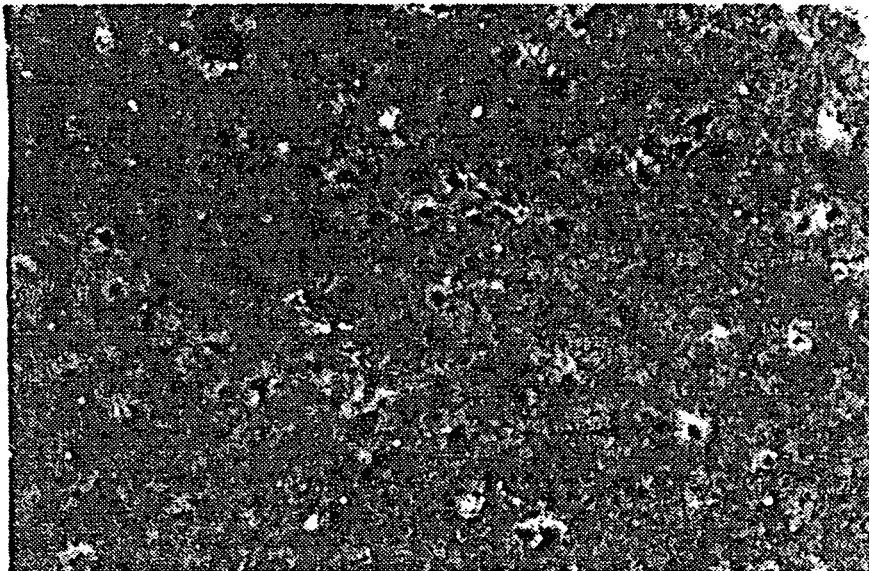


FIG. 27B



European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 04 07 6254

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
A	CACERES A ET AL: "The effect of tau antisense oligonucleotides on neurite formation of cultured cerebellar macroneurons." J NEUROSCI, JUN 1991, 11 (6) P1515-23, June 1991 (1991-06), XP000604108 UNITED STATES * the whole document *	47	C12N15/12 G01N33/53 A61K49/00 A61K31/70 C12Q1/68 C12N5/00 C12P21/02 C07H15/12
Y	JOACHIM C L ET AL: "Amyloid [beta]-protein deposition in tissue other than brain in Alzheimer's disease" NATURE 1989 UNITED KINGDOM, vol. 341, no. 6239, 1989, pages 226-230, XP002326757 ISSN: 0028-0836 * the whole document *	1-49	
Y	JOHNSON S A ET AL: "Relation of neuronal APP-751/APP-695 mRNA ratio and neuritic plaque density in Alzheimer's disease" SCIENCE 1990 UNITED STATES, vol. 248, no. 4957, 1990, pages 854-857, XP001206274 ISSN: 0036-8075 * the whole document *	1-49	TECHNICAL FIELDS SEARCHED (Int.Cl.7) C07K
Y	GUTIERREZ A A ET AL: "Gene therapy for cancer" LANCET 1992 UNITED KINGDOM, vol. 339, no. 8795, 1992, pages 715-721, XP002940794 ISSN: 0140-6736 * the whole document *	1-49	
The present search report has been drawn up for all claims			
Place of search Munich		Date of completion of the search 31 May 2005	Examiner Loubradou-Bourges, N
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p>			

5
EPO FORM 1503 03.02 (P04C01)